WEST Search History

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DATE: Thursday, April 12, 2007

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT; PLUR=YES; OP=OR		
☐	L15	predict near3 side adj effect same profile same trea$ same (diseas$ or patho$)	4
☐	L14	L13 and (diseas$ or patho$)	9
☐	L13	predict near3 side adj effect same profile same trea$	10
☐	L12	l8 and L10	0
☐	L11	l3 and L10	0
☐	L10	predict near3 side adj effect	172
☐	L9	predict near3 side adj effect and l3	0
☐	L8	effec$ near5 trea$ same trea$ with (diseas$ or patho$) with array same profile	5
☐	L7	l3 and L6	46
☐	L6	effec$ near5 trea$	255769
☐	L5	trea$ with (diseas$ or patho$) near5 (tissue or sample or cell) with array same profile	5
☐	L4	trea$ with (diseas$ or patho$) near5 (tissue or sample) with array same profile	4
☐	L3	trea$ with (diseas$ or patho$) with array same profile	71
☐	L2	20030049701.pn.	1
☐	L1	10/640081	3

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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	DEC 18	CA/CAplus pre-1967 chemical substance index entries enhanced with preparation role
NEWS 4	DEC 18	CA/CAplus patent kind codes updated
NEWS 5	DEC 18	MARPAT to CA/CAplus accession number crossover limit increased to 50,000
NEWS 6	DEC 18	MEDLINE updated in preparation for 2007 reload
NEWS 7	DEC 27	CA/CAplus enhanced with more pre-1907 records
NEWS 8	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS 9	JAN 16	CA/CAplus Company Name Thesaurus enhanced and reloaded
NEWS 10	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS 11	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS 12	JAN 22	CA/CAplus updated with revised CAS roles
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NEWS 14	JAN 29	PHAR reloaded with new search and display fields
NEWS 15	JAN 29	CAS Registry Number crossover limit increased to 300,000 in multiple databases
NEWS 16	FEB 15	PATDPASPC enhanced with Drug Approval numbers
NEWS 17	FEB 15	RUSSIAPAT enhanced with pre-1994 records
NEWS 18	FEB 23	KOREAPAT enhanced with IPC 8 features and functionality
NEWS 19	FEB 26	MEDLINE reloaded with enhancements
NEWS 20	FEB 26	EMBASE enhanced with Clinical Trial Number field
NEWS 21	FEB 26	TOXCENTER enhanced with reloaded MEDLINE
NEWS 22	FEB 26	IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS 23	FEB 26	CAS Registry Number crossover limit increased from 10,000 to 300,000 in multiple databases
NEWS 24	MAR 15	WPIDS/WPIX enhanced with new FRAGHITSTR display format
NEWS 25	MAR 16	CASREACT coverage extended
NEWS 26	MAR 20	MARPAT now updated daily
NEWS 27	MAR 22	LWPI reloaded
NEWS 28	MAR 30	RDISCLOSURE reloaded with enhancements
NEWS 29	MAR 30	INPADOCDB will replace INPADOC on STN
NEWS 30	APR 02	JICST-EPLUS removed from database clusters and STN

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NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS LOGIN	Welcome Banner and News Items
NEWS IPC8	For general information regarding STN implementation of IPC 8
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FILE 'HOME' ENTERED AT 14:06:06 ON 12 APR 2007

=> medline biosis caplus scisearch embase
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Some commands only work in certain files. For example, the EXPAND command can only be used to look at the index in a file which has an index. Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of commands which can be used in this file.

=> fil medline biosis caplus scisearch embase

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.84	0.84

FILE 'MEDLINE' ENTERED AT 14:08:17 ON 12 APR 2007

FILE 'BIOSIS' ENTERED AT 14:08:17 ON 12 APR 2007
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=> gene and profile and expres? and correl and review
MISSING TERM BEFORE 'AND'
Search expressions cannot begin with operators.

=> gene and profile and expres? and correl? and review
L1 193 GENE AND PROFILE AND EXPRES? AND CORREL? AND REVIEW

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2 133 DUP REM L1 (60 DUPLICATES REMOVED)

=> t ti l2 1-50

L2 ANSWER 1 OF 133 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
TI [Aberrant methylation of tumor suppressor genes in head and neck squamous cell carcinoma: Is it clinically relevant?].
LA METHYLATION DES GENES SUPPRESSEURS DE TUMEUR DANS LES CANCERS DES VOIES AERODIGESTIVES SUPERIEURES: QUELLE SIGNIFICATION CLINIQUE?.

L2 ANSWER 2 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Implications of micro-RNA profiling for cancer diagnosis

L2 ANSWER 3 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Genomics and Proteomics of Bone Cancer

L2 ANSWER 4 OF 133 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
TI Genomics and proteomics of bone cancer.

L2 ANSWER 5 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 1
TI Complementary analysis of microsatellite tumor profile and mismatch defects in colorectal carcinomas

L2 ANSWER 6 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 2
TI Multiple sclerosis therapy monitoring based on gene expression

L2 ANSWER 7 OF 133 MEDLINE on STN DUPLICATE 3
TI Distinctiveness of secretory phospholipase A2 group IIA and V suggesting unique roles in atherosclerosis.

L2 ANSWER 8 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 4
TI Bridging behavior and physiology: ion-channel perspective on mushroom body-dependent olfactory learning and memory in Drosophila

L2 ANSWER 9 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Microarray data on gene modulation by HIV-1 in immune cells: 2000-2006

L2 ANSWER 10 OF 133 MEDLINE on STN DUPLICATE 5
TI Microarrays in breast cancer research and clinical practice--the future lies ahead.

L2 ANSWER 11 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Soluble osteogenic molecular signals and the induction of bone formation

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TI Gene expression profile of idiopathic thrombocytopenic purpura (ITP).

L2 ANSWER 13 OF 133 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN DUPLICATE 6
TI Advances in congenital long QT syndrome

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TI Tic disorders and obsessive-compulsive disorder: Is autoimmunity involved?.

L2 ANSWER 15 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Gene expression profiling of thyroid tumors- clinical applicability

L2 ANSWER 16 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Integrating genetic and gene expression data: application to cardiovascular and metabolic traits in mice

L2 ANSWER 17 OF 133 MEDLINE on STN
TI Studying multiple protein profiles over time to assess biomarker validity.

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TI Gene expression profile assays as predictors
of recurrence-free survival in early-stage breast cancer: A metaanalysis.

L2 ANSWER 20 OF 133 MEDLINE on STN DUPLICATE 7
TI Microarrays as validation strategies in clinical samples: tissue and protein microarrays.

L2 ANSWER 21 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Thymus-dependent T cell tolerance of neuroendocrine functions principles, reflections, and implications for tolerogenic/negative self-vaccination

L2 ANSWER 22 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Establishment of cell lines that exhibit correct ontogenic stage-specific gene expression profiles from tissues of yeast
artificial chromosome transgenic mice using chemically induced growth signals

L2 ANSWER 23 OF 133 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
TI Adipose tissue: Something more than just adipocytes.

L2 ANSWER 24 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Molecular approaches to chronic kidney disease

L2 ANSWER 25 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 8
TI Prognosis of follicular lymphomas

L2 ANSWER 26 OF 133 MEDLINE on STN DUPLICATE 9
TI Molecular profiling of breast cancer.

L2 ANSWER 27 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Advancement in characterization of genomic alterations for improved diagnosis, treatment and prognostics in cancer

L2 ANSWER 28 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Gene expression profiling for prediction of response
to chemotherapy

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TI Identification and functional analysis of damage-induced neuronal endopeptidase (DINE), a nerve injury associated molecule.

L2 ANSWER 30 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Can the state of cancer chemotherapy resistance be reverted by epigenetic therapy?

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TI Role of genomic markers in colorectal cancer treatment

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TI Improving molecular cancer class discovery through sparse non-negative matrix factorization.

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TI Genomic medicine: genetic variation and its impact on the future of health care

L2 ANSWER 34 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Microarray-based functional protein profiling using peptide nucleic acid-encoded libraries

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TI Pharmacogenomics in colorectal carcinomas: Future perspectives in personalized therapy

L2 ANSWER 36 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI The importance of colonic butyrate transport to the regulation of genes associated with colonic tissue homeostasis

L2 ANSWER 37 OF 133 MEDLINE on STN DUPLICATE 10
TI The use of transcriptomics to address questions in behaviour: production of a suppression subtractive hybridisation library from dominance hierarchies of rainbow trout.

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TI What is needed for effective antitumor immunotherapy? Lessons learned using Listeria monocytogenes as a live vector for HPV-associated tumors.

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TI Complex diseases in gastroenterology and hepatology: GERD, Barrett's and esophageal adenocarcinoma

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TI Protein profiles associated with experimental duodenal ulcer in rats.

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TI Harnessing the power of gene microarrays for the study of brain aging and Alzheimer's disease: Statistical reliability and functional correlation

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TI Renal localization, expression, and developmental regulation of P450 4F cytochromes in three substrains of spontaneously hypertensive rats.

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TI Gene profiling of high risk neuroblastoma.

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TI Down syndrome, Alzheimer's disease and seizures.

L2 ANSWER 46 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI "Promoter array" studies identify cohorts of genes directly regulated by methylation, copy number change, or transcription factor binding in human cancer cells

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TI Genomic and gene expression signature of the pre-invasive testicular carcinoma in situ.

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TI Melanocyte and keratinocyte carcinogenesis: p53 family protein activities and intersecting mRNA expression profiles

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TI The role of interferon-gamma on immune and allergic responses

L2 ANSWER 50 OF 133 CAPLUS COPYRIGHT 2007 ACS on STN
TI Immunotherapeutic potential of DISC-HSV and OX40L in cancer

=> d his

(FILE 'HOME' ENTERED AT 14:06:06 ON 12 APR 2007)

FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE' ENTERED AT 14:08:17 ON 12 APR 2007
L1 193 GENE AND PROFILE AND EXPRES? AND CORREL? AND REVIEW
L2 133 DUP REM L1 (60 DUPLICATES REMOVED)

=> (array or ?array) and l2
L3 47 (ARRAY OR ?ARRAY) AND L2

=> t ti l3 1-47

L3 ANSWER 1 OF 47 MEDLINE on STN
TI Microarrays in breast cancer research and clinical practice--the future lies ahead.

L3 ANSWER 2 OF 47 MEDLINE on STN
TI Microarrays as validation strategies in clinical samples: tissue and protein microarrays.

L3 ANSWER 3 OF 47 MEDLINE on STN
TI Molecular profiling of breast cancer.

L3 ANSWER 4 OF 47 MEDLINE on STN
TI The use of transcriptomics to address questions in behaviour: production of a suppression subtractive hybridisation library from dominance hierarchies of rainbow trout.

L3 ANSWER 5 OF 47 MEDLINE on STN
TI Genetics in renal cell carcinoma.

L3 ANSWER 6 OF 47 MEDLINE on STN
TI Classification of follicular thyroid tumors by molecular signature: results of gene profiling.

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TI Protein profiles associated with experimental duodenal ulcer in rats.

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TI Gene expression profile signatures to predict survival in diffuse large B-cell lymphoma: A meta-analysis of early results.

L3 ANSWER 9 OF 47 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI Gene expression profiling (GEP) in de novo pediatric acute myeloid leukemia (AML) patients reveals a robust expression signature that correlates with inv(16) and t(16;16).

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TI Genetic profiling and microarray technology.

L3 ANSWER 11 OF 47 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
TI DNA chips in medicine and science.

L3 ANSWER 12 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Microarray data on gene modulation by HIV-1 in immune cells: 2000-2006

L3 ANSWER 13 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Multiple sclerosis therapy monitoring based on gene expression

L3 ANSWER 14 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Genomics and Proteomics of Bone Cancer

L3 ANSWER 15 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Gene expression profiling of thyroid tumors- clinical applicability

L3 ANSWER 16 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI "Promoter array" studies identify cohorts of genes directly regulated by methylation, copy number change, or transcription factor binding in human cancer cells

L3 ANSWER 17 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Gene expression profiling for prediction of response to chemotherapy

L3 ANSWER 18 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Microarray-based functional protein profiling using peptide nucleic acid-encoded libraries

L3 ANSWER 19 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Melanocyte and keratinocyte carcinogenesis: p53 family protein activities and intersecting mRNA expression profiles

L3 ANSWER 20 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Estrogen signaling and prediction of endocrine therapy

L3 ANSWER 21 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI The results of the expression array studies correlate and enhance the known genetic basis of gastric and colorectal cancer

L3 ANSWER 22 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI From microarray to biological networks: Analysis of gene expression profiles

L3 ANSWER 23 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Genomic medicine: genetic variation and its impact on the future of health care

L3 ANSWER 24 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI The importance of colonic butyrate transport to the regulation of genes associated with colonic tissue homeostasis

L3 ANSWER 25 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Gene expression pattern of obese and control individuals in adipose tissue and peripheral blood mononuclear cells

L3 ANSWER 26 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

TI Artificial neural network technologies to identify biomarkers for therapeutic intervention

L3 ANSWER 27 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Analysis of gastric cancer with cDNA microarray

L3 ANSWER 28 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI What do microarrays really tell us about M. tuberculosis?

L3 ANSWER 29 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI A comparison of global gene expression measurement technologies in Arabidopsis thaliana

L3 ANSWER 30 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Effect of agonal and postmortem factors on gene expression profile: quality control in microarray analyses of postmortem human brain

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TI Gene expression profiling in childhood acute leukemia: progress and perspectives

L3 ANSWER 32 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Understanding cancer through gene expression profiling

L3 ANSWER 33 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Mapping stresses in Escherichia coli to improve yield

L3 ANSWER 34 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
TI Glucose-regulated gene expression maintaining the glucose-responsive state of β-cells

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TI Gene expression profiles for monitoring radiation exposure

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TI Protein microarrays - a tool for the post-genomic era

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TI Harnessing the power of gene microarrays for the study of brain aging and Alzheimer's disease: Statistical reliability and functional correlation

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TI A gene expression fingerprint of C. elegans embryonic motor neurons.

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TI Asiaticoside induction for cell-cycle progression, proliferation and collagen synthesis in human dermal fibroblasts.

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TI How much expression divergence after yeast gene duplication could be explained by regulatory motif evolution?.

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TI Customized antigens for desensitizing allergic patients.

=> d ibib abs 1-47 l3

L3 ANSWER 1 OF 47 MEDLINE on STN
ACCESSION NUMBER: 2006719789 MEDLINE
DOCUMENT NUMBER: PubMed ID: 17158752
TITLE: Microarrays in breast cancer research and clinical practice--the future lies ahead.
AUTHOR: Gruvberger-Saal Sofia K; Cunliffe Heather E; Carr Kristen M; Hedenfalk Ingrid A
CORPORATE SOURCE: Institute for Cancer Genetics, Columbia University, New York, New York 10032, and New York Presbyterian Hospital, New York, NY 10021, USA.
SOURCE: Endocrine-related cancer, (2006 Dec) Vol. 13, No. 4, pp. 1017-31. Ref: 97
Journal code: 9436481. ISSN: 1351-0088.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200703
ENTRY DATE: Entered STN: 13 Dec 2006
Last Updated on STN: 2 Mar 2007
Entered Medline: 1 Mar 2007
AB Molecular profiling for classification and prognostic purposes has demonstrated that the genetic signatures of tumors contain information regarding biological properties as well as clinical behavior. This review highlights the progress that has been made in the field of gene expression profiling of human breast cancer.
Breast cancer has become one of the most intensely studied human malignancies in the genomic era; several hundred papers over the last few

years have investigated various clinical and biological aspects of human breast cancer using high-throughput molecular profiling techniques. Given the grossly heterogeneous nature of the disease and the lack of robust conventional markers for disease prediction, prognosis, and response to treatment, the notion that a transcriptional profile comprising multiple genes, rather than any single gene or other parameter, will be more predictive of tumor behavior is both appealing and reasonable. Promising results have emerged from these studies, correlating gene expression profiles with prognosis, recurrence, metastatic potential, therapeutic response, as well as biological and functional aspects of the disease. Clearly, the integration of genomic approaches into the clinic lies in the near future, but prospective studies based on larger patient cohorts representing the whole spectrum of breast cancer, oncogenic pathway-based studies, attendant care in bioinformatic analyses and validation studies are needed before the full promise of gene expression profiling can be realized in the clinical setting.

L3 ANSWER 2 OF 47 MEDLINE on STN
ACCESSION NUMBER: 2006635916 MEDLINE
DOCUMENT NUMBER: PubMed ID: 17069510
TITLE: Microarrays as validation strategies in clinical samples: tissue and protein microarrays.
AUTHOR: Aguilar-Mahecha Adriana; Hassan Saima; Ferrario Cristiano; Basik Mark
CORPORATE SOURCE: Montreal Center for Experimental Therapeutics in Cancer, Lady Davis Institute for Medical Research, The Sir Mortimer B. Davis-Jewish General Hospital, and Department of Oncology, McGill University and Surgery, Montreal, Canada.
SOURCE: Omics : a journal of integrative biology, (2006 Fall) Vol. 10, No. 3, pp. 311-26. Ref: 111
Journal code: 101131135. ISSN: 1536-2310.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(VALIDATION STUDIES)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200612
ENTRY DATE: Entered STN: 31 Oct 2006
Last Updated on STN: 19 Dec 2006
Entered Medline: 15 Dec 2006

AB The widespread use of DNA microarrays has led to the discovery of many genes whose expression profile may have significant clinical relevance. The translation of this data to the bedside requires that gene expression be validated as protein expression, and that annotated clinical samples be available for correlative and quantitative studies to assess clinical context and usefulness of putative biomarkers. We review two microarray platforms developed to facilitate the clinical validation of candidate biomarkers: tissue microarrays and reverse-phase protein microarrays. Tissue microarrays are arrays of core biopsies obtained from paraffin-embedded tissues, which can be assayed for histologically-specific protein expression by immunohistochemistry. Reverse-phase protein microarrays consist of arrays of cell lysates or, more recently, plasma or serum samples, which can be assayed for protein quantity and for the presence of post-translational modifications such as phosphorylation. Although these platforms are limited by the availability of validated antibodies, both enable the preservation of precious clinical samples as well as experimental standardization in a high-throughput manner proper to microarray technologies. While tissue microarrays are rapidly becoming a mainstay of translational research, reverse-phase protein microarrays require further

technical refinements and validation prior to their widespread adoption by research laboratories.

L3 ANSWER 3 OF 47 MEDLINE on STN
ACCESSION NUMBER: 2006105870 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 16493262
TITLE: Molecular profiling of breast cancer.
AUTHOR: Paik Soonmyung
CORPORATE SOURCE: Division of Disease, NSABP Foundation, Pittsburgh, Pennsylvania, USA.
SOURCE: Current opinion in obstetrics & gynecology, (2006 Feb) Vol. 18, No. 1, pp. 59-63.
Journal code: 9007264. ISSN: 1040-872X.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: NONMEDLINE; IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 23 Feb 2006
Last Updated on STN: 12 Dec 2006

AB PURPOSE OF REVIEW: This review is a comprehensive survey of molecular-profiling literature published since 2004. RECENT FINDINGS: More microarray-based gene-expression profiles that are prognostic for breast cancer have been published, strengthening the possibility that the microarray gene-expression profile may indeed provide clinically meaningful results. Requirement for snap-frozen tissue, however, will continue to be a limiting factor in clinical application. Results from a multicenter validation study were less spectacular than the original findings. A prognostic model based on classical markers performed well in a comparative study. Further clinical validation, with a large sample size, is needed. A prognostic gene-expression profile of 21 genes, which can be assayed using routinely processed formalin-fixed paraffin-embedded tumor tissue, has been introduced and this assay has also been shown to correlate with degree of benefit from chemotherapy. Two large clinical trials to validate gene-expression-based assays are to be launched in North America (TAILORx) and the European Union (MINDACCT). The usefulness of these genomic tools is still being debated, because clinicopathologic factors also are still important. SUMMARY: Gene-expression-based prognostic tests are now available as commercial reference laboratory tests. Their successful implementation will depend on the seamless integration with existing clinicopathologic markers.

L3 ANSWER 4 OF 47 MEDLINE on STN
ACCESSION NUMBER: 2005430169 MEDLINE
DOCUMENT NUMBER: PubMed ID: 16052453
TITLE: The use of transcriptomics to address questions in behaviour: production of a suppression subtractive hybridisation library from dominance hierarchies of rainbow trout.
AUTHOR: Sneddon Lynne U; Margareto Javier; Cossins Andrew R
CORPORATE SOURCE: School of Biological Sciences, BioScience Building, University of Liverpool, Liverpool L69 7ZB, United Kingdom.. lsneddon@liv.ac.uk
SOURCE: Physiological and biochemical zoology : PBZ, (2005 Sep-Oct) Vol. 78, No. 5, pp. 695-705. Electronic Publication: 2005-07-28.
Journal code: 100883369. ISSN: 1522-2152.
PUB. COUNTRY: United States
DOCUMENT TYPE: (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)

(RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200605
ENTRY DATE: Entered STN: 15 Aug 2005
Last Updated on STN: 3 May 2006
Entered Medline: 2 May 2006

AB Microarrays, or gene chips, are transforming the way that gene expression is measured by allowing us to determine the expression of thousands of genes from a sample. This gives immense power to examine gene expression on a global scale within individual animals and between animals. The scope for analysing complex animal functions at the molecular level is within our grasp. Relatively few studies have examined complex behaviours and correlated them with gene expression in the central nervous system. Here, we review the use of microarray technology in the dissection of behaviour and focus specifically on dominance status. A cDNA library using suppression subtraction hybridisation on rainbow trout Oncorhynchus mykiss of differing status has been produced to enrich the cDNA library for genes that are differentially expressed between individuals of different dominance status. A preliminary analysis demonstrated that there were 1,165 genes that differed between fish of different dominance status. Therefore, there is the potential of correlating gene expression profile with rank position within dominance hierarchies, thus identifying targets for candidate gene approaches.

L3 ANSWER 5 OF 47 MEDLINE on STN
ACCESSION NUMBER: 2003480951 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14560139
TITLE: Genetics in renal cell carcinoma.
AUTHOR: Dal Cin Paola
CORPORATE SOURCE: Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts, USA.. pdalcin@partners.org
SOURCE: Current opinion in urology, (2003 Nov) Vol. 13, No. 6, pp. 463-6. Ref: 25
Journal code: 9200621. ISSN: 0963-0643.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200408
ENTRY DATE: Entered STN: 16 Oct 2003
Last Updated on STN: 1 Sep 2004
Entered Medline: 31 Aug 2004

AB PURPOSE OF REVIEW: The combination of several recent molecular technologies, including comparative genomic hybridization, fluorescence in-situ hybridization and complementary DNA and tissue microarrays, has advanced our understanding of renal cancer. However, a great deal of information regarding the genetics of renal neoplasms has also emerged from the extensive cytogenetic investigations in the past decade. RECENT FINDINGS: The correlation between cytogenetic or molecular genetic abnormalities and histomorphology is most consistent in clear cell and papillary types of renal cell carcinoma. However, gene expression profile studies have brought new insights into the classification of renal tumors, and may provide new markers that identify patients with a poor prognosis as well as identifying potential therapeutic targets. SUMMARY: The integration of expression profile data and clinical parameters could serve to enhance the diagnosis and prognosis of renal cell carcinoma. The identification and evaluation of new molecular parameters will be necessities in cancer

research and cancer treatment.

L3 ANSWER 6 OF 47 MEDLINE on STN
ACCESSION NUMBER: 2003217166 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12738736
TITLE: Classification of follicular thyroid tumors by molecular signature: results of gene profiling.
AUTHOR: Barden Catherine B; Shister Katherine W; Zhu Baixin; Guiter Gerardo; Greenblatt David Y; Zeiger Martha A; Fahey Thomas J 3rd
CORPORATE SOURCE: Department of Surgery, New York Presbyterian Hospital and Weill Medical College of Cornell University, New York 10021, USA.
SOURCE: Clinical cancer research : an official journal of the American Association for Cancer Research, (2003 May) Vol. 9, No. 5, pp. 1792-800.
Journal code: 9502500. ISSN: 1078-0432.
PUB. COUNTRY: United States
DOCUMENT TYPE: (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200401
ENTRY DATE: Entered STN: 13 May 2003
Last Updated on STN: 13 Jan 2004
Entered Medline: 12 Jan 2004

AB PURPOSE: Thyroid nodules are common, with a lifetime risk of developing a clinically significant thyroid nodule of 10% or higher. Preoperative diagnosis was greatly enhanced by the introduction of fine needle aspiration in the 1970s, but there has been little advancement since that time. Discrimination between benign and malignant follicular neoplasms is currently not possible by fine needle aspiration and can even be difficult after full pathologic review. The purpose of these studies is to identify genes expressed in follicular adenomas and carcinomas of the thyroid that will permit molecular differentiation of these neoplasms. Experimental Design: Gene expression patterns of 17 thyroid follicular tumors were analyzed by oligonucleotide array analysis. Gene profiles for follicular adenomas and carcinomas were identified, and the two groups were compared for differences in expression levels. The differentially expressed genes were used to perform a hierarchical clustering analysis training set. Five follicular tumors with diagnosis undisclosed to the investigators and 2 minimally invasive carcinomas were entered into the cluster analysis as a test set to determine whether diagnosis by gene profile correlated with that obtained by pathologic evaluation. RESULTS: Thyroid follicular adenomas and carcinomas showed strikingly distinct gene expression patterns. The expression patterns of 105 genes were found to be significantly different between follicular adenoma and carcinoma. Many uncharacterized genes contributed to the distinction between tumor types. For five follicular tumors for which the final diagnosis was undisclosed, the clustering algorithm gave the correct diagnosis in all 5 cases. CONCLUSIONS: Gene profiling is a useful tool to predict the molecular diagnosis of follicular thyroid tumors. Genes were identified that reliably differentiate follicular thyroid carcinoma from adenoma. This study provides insight into genes that may be important in the molecular pathogenesis of follicular thyroid tumors, as well candidates for preoperative diagnosis of follicular thyroid carcinoma.

L3 ANSWER 7 OF 47 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2005:530505 BIOSIS
DOCUMENT NUMBER: PREV200510324020

TITLE: Protein profiles associated with experimental duodenal ulcer in rats.
AUTHOR(S): Khomenko, Tetyana [Reprint Author]; Deng, Xiaorning; Sandor, Zsuzsanna; Osapay, Klara; Heck, Denis J.; Szabo, Sandor
CORPORATE SOURCE: Univ Calif Irvine, VA Med Ctr, Long Beach, CA 90822 USA
SOURCE: FASEB Journal, (MAR 4 2005) Vol. 19, No. 4, Suppl. S, Part 1, pp. A493.
Meeting Info.: Experimental Biology 2005 Meeting/35th International Congress of Physiological Sciences. San Diego, CA, USA. March 31 -April 06, 2005. Amer Assoc Anatomists; Amer Assoc Immunologists; Amer Physiol Soc; Amer Soc Biochem & Mol Biol; Amer Soc Investigat Pathol; Amer Soc Nutr Sci; Amer Soc Pharmacol & Expt Therapeut; Int Union Physiol Sci.
CODEN: FAJOEC. ISSN: 0892-6638.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 1 Dec 2005
Last Updated on STN: 1 Dec 2005

AB Recently we identified ulcer-associated genes in the duodenal mucosa, using gene microarray technologies, in the early stage of duodenal ulcers induced by cysteamine (C) in rats. Now we used BD Clontech (TM) Ab Microarray 500 to monitor the differential expression of about 500 proteins.Methods: Unfasted Sprague-Dawley rats (150-180g) were given C (25 mg/100g) by gavage, and protein profile in duodenal mucosa was detected 0.5 and 6.0 hr later.Results: A good correlation with gene microarray data was found in the expressions of both cytosolic and membrane proteins which represent a broad range of biological functions including gene transcription, cell-cycle regulation, signal transduction and apoptosis. Statistical analysis showed that C increased the expression of 8 and 26 proteins, but inhibited the expression of 11 and 21 proteins at 0.5 and 6 hr, respectively. C induced a prominent upregulation of CTBP1 (C-terminal binding protein 1), GABA b R2, Erg-2 (potassium voltage-gatedchannel), prenylcysteine oxidase 1, ezrin, E2F, NFAT-1, p21, CRIP2 (cysteine-rich protein 2), calcineurin, caspase-7, COX-2, synuclein-1 and down-regulation of RPTPb, PTP1D/SHP2, Cyclin A, EGF Receptor, Hsp 90, Sos1, tomosyn.Conclusion: An array-based approach for the determination of protein profiles may facilitate the identification of new proteins associated with duodenal ulcer disease. (Supported by VA Merit Review grant).

L3 ANSWER 8 OF 47 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2005:478341 BIOSIS
DOCUMENT NUMBER: PREV200510270245
TITLE: Gene expression profile signatures to predict survival in diffuse large B-cell lymphoma: A meta-analysis of early results.
AUTHOR(S): Lyman, Gary H. [Reprint Author]; Kuderer, Nicole M.
CORPORATE SOURCE: Univ Rochester, Sch Med and Dent, Rochester, NY USA
SOURCE: Blood, (NOV 16 2004) Vol. 104, No. 11, Part 1, pp. 626A.
Meeting Info.: 46th Annual Meeting of the American-Society-of-Hematology. San Diego, CA, USA. December 04 -07, 2004. Amer Soc Hematol.
CODEN: BLOOAW. ISSN: 0006-4971.
DOCUMENT TYPE: Conference; (Meeting)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 16 Nov 2005
Last Updated on STN: 16 Nov 2005

AB Background: Diffuse large B-cell lymphoma (DLBCL) represents the most common lymphoma in adults. Although responsive to chemotherapy, less than half of patients are currently cured. In an effort to better assess prognosis, several investigators have attempted to define gene expression signatures based on their prediction of survival. The preliminary analysis reported here is part of an ongoing effort to systematically review and catalogue classes and test performance characteristics of reported gene expression signatures in patients with DLBCL. Methods: All reports of gene expression profiling in patients with DLBCL were sought through an extensive search of the published literature including MEDLINE, EMBASE, the Cochrane Library and hand searching of references. Elevenreported studies in patients with DLBCL were identified which reported the relationship between a gene expression signature and overall survival. Weighted summary measures of test performance were estimated including sensitivity, specificity, likelihood ratio, posttest probability (PP) and the diagnostic odds ratio (DOR) as an overall measure of test discrimination. An inconsistency index (I-2) was used to reflect the proportion of variation in estimates due to heterogeneity. Seven studies also provided signature results stratified by International Prognostic Index (IPI). Results: Reported series included 1027 patients ranging from 22 to 240 per study. Five studies utilized cross validation techniques while six were based on independent cohorts. Five-year survivals were 28% and 69% among the 501 high-risk profile and 525 low-risk patients, respectively. Summary gene expression signature performance characteristics for survival are shown:[GRAPHICS]The estimated I-2 was 43%. The false negative rate and false positive rate were over 20% in 7 (64%) and 9 (82%) of studies, respectively. Althoughnot reaching statistical significance, test performance measures were generally poorer in studies with independent validation. The number of genes in the assay correlated inversely with the DOR [r(sp) = 0.59, p=.05], the likelihood ratio negative [r(sp) = 0.70, p=.02] and the posttest probability negative [r(sp) = .78, p<.01]. Among reporting studies, 263 patients were IPI high and 374 IPI low-risk. The 5-year survival rate among IPI high risk patients were 8% and 52% in high and low risk profile subjects, respectively. Likewise, among IPI low risk patients, 5-year survival of 46% and 81% were observed among high and low risk profile patients. The DOR of the gene expression signatures among IPI low risk and high-risk patients were 6.66 [3.15,14.07] and 10.98 [5.51, 21.89], respectively. Discussion: Gene expression profiling based on microarray analysis shows early promise for improving clinicalestimation of survival in patients with DLBCL. However, the use of these assays in therapeutic decision-making must consider both the limitations of assay test performance and the specific patient population being evaluated.

L3 ANSWER 9 OF 47 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:140651 BIOSIS

DOCUMENT NUMBER: PREV200400133831

TITLE: Gene expression profiling (GEP) in de novo pediatric acute myeloid leukemia (AML) patients reveals a robust expression signature that correlates with inv(16) and t(16;16).

AUTHOR(S): Lacayo, Norman [Reprint Author]; Kinnunen, Paivi [Reprint Author]; Raimondi, Susana C.; Yu, Ron; Wahab, Romina; Stuber, Christianna; Douglas, Lorrie; Chang, Myron; Willman, Cheryl L.; Ravindranath, Yaddanapuddi; Weinstein, Howard; Becton, David; Behm, Fred; Tibshirani, Robert; Sikic, Branimir I.; Dahl, Gary V. [Reprint Author]

CORPORATE SOURCE: Pediatrics, Division of Hematology-Oncology, Stanford University, Stanford, CA, USA

SOURCE: Blood, (November 16 2003) Vol. 102, No. 11, pp. 365a.

print.
Meeting Info.: 45th Annual Meeting of the American Society of Hematology. San Diego, CA, USA. December 06-09, 2003. American Society of Hematology.
CODEN: BLOOAW. ISSN: 0006-4971.

DOCUMENT TYPE: Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 10 Mar 2004
Last Updated on STN: 10 Mar 2004

AB To explore the use of GEP as a tool to evaluate molecular subgroups in childhood AML we studied the relationship between GEP and inv(16) and t(16;16) chromosomal abnormalities, a known good risk feature present in approximately 6% of pediatric AML cases. Bone marrow samples from 104 de novo and relapsed patients with childhood AML registered on the Pediatric Oncology Group (POG) study 9421 were analyzed with 43,760 element spotted arrays (containing 41,751 unique genes and ESTs) from the Stanford University Microarray Core Facility. Cytogenetic testing was carried out by clinical laboratories at institutions where patients were diagnosed; all cytogenetic reports underwent centralized review. Of the 104 diagnostic samples, 27 manifested inv(16) or t(16;16) on standard cytogenetic analysis and of these 26 yielded intact RNA. An expression signature that correctly predicted the presence of inv(16) or t(16;16) was identified. First, we used the Significance Analysis of Microarrays (SAM) (Tusher, Tibshirani and Chu, PNAS 2001, 98:5116-5121) to examine differences in the gene expression between samples with and without inv(16) and t(16;16) and identified a list of 157 differentially expressed genes (RUNX3, PBX3, ZNF274A, CD81 antigen, TESS-2, and CBF/B). Next, we used the Prediction Analysis for Microarrays (PAM) (Tibshirani, Hastie, Narashiman and Chu, PNAS 2002, 99:6567-6572) to find the minimum number of genes that could identify the inv(16) and t(16;16) samples. A set of 397 genes accurately identified all samples harboring inv(16) or t(16;16) chromosomal abnormality with a cross-validated probability of 100% (overall misclassification error rate 13%) in comparison to samples with 11q23 and miscellaneous cytogenetics. Genes found to be over-expressed included: CDC37 homolog, CDD, AXL oncogene, KRML and MKP3. Genes found to be under-expressed included: SET, B-IND1, Cyclin C, T-box protein 2 and oncogene YES-1. In summary, GEP identifies a signature for the inv(16)/t(16;16) cytogenetic abnormality. Ongoing analysis with a larger subset of samples may identify a GEP predictive of clinical outcomes and identify patients with inv(16)/t(16;16) who may have a higher risk of relapse and therefore may need more intensive post-remission chemotherapy. By identifying an expression profile for the higher risk patients with inv(16)/t(16;16) matched related donor bone marrow transplantation in first remission may be avoided in the lower risk patients. In addition, we are also analyzing whether or not the robust GEP seen in patients with inv(16)/t(16;16) is shared by other childhood AML patients with good outcome in the POG study 9421.

L3 ANSWER 10 OF 47 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2002:136519 BIOSIS
DOCUMENT NUMBER: PREV200200136519
TITLE: Genetic profiling and microarray technology.
AUTHOR(S): Albertsen, Hans [Reprint author]
CORPORATE SOURCE: Amersham Pharmacia Biotech, 928 E. Arques Ave., Sunnyvale, CA, 94086, USA
Hans.Albertsen@am.APBiotech.com
SOURCE: Journal of Clinical Ligand Assay, (Winter, 2000) Vol. 23, No. 4, pp. 283-292. print.

ISSN: 1081-1672.
DOCUMENT TYPE: Article
General Review; (Literature Review)
LANGUAGE: English
ENTRY DATE: Entered STN: 6 Feb 2002
Last Updated on STN: 26 Feb 2002

AB Over the past few years gene expression profiling has become a key element of the quest to better understand gene function and cellular behavior. An expression profile can be measured either on the protein level, which is difficult given the limitations of current technologies, or it can be measured on the mRNA level. The fundamental assumption behind using the mRNA approach to elucidate cellular function is that abundance of a specific mRNA species is correlated with the abundance of the protein it encodes. It follows from this assumption that the profile of transcribed mRNA indirectly dictates function and behavior of the cell. Any changes in expression profiles are likely to cause changes in cellular functionality or behavior; but biologic characteristics like tissue type and cellular state would influence the expression profile in the first place. While the correlation between expression profile and phenotype is likely to be true, it must be emphasized that the relationship is highly complex and that our understanding of this correlation is in its infancy. Various strategies have been devised to assess gene expression profiles in a quantitative manner and, judged by today's standards, microarray technology appears to provide the most direct and comprehensive approach. This review describes microarray technology and its applications in drug discovery and in characterization of diseases.

L3 ANSWER 11 OF 47 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2000:123056 BIOSIS
DOCUMENT NUMBER: PREV200000123056
TITLE: DNA chips in medicine and science.
AUTHOR(S): Lee, Peter; Hudson, Thomas J. [Reprint author]
CORPORATE SOURCE: Centre genomique de Montreal, Universite McGill, 1650, Cedar avenue, Montreal, Quebec, H3G 1A4, Canada
SOURCE: M-S (Medecine Sciences), (jAN., 2000) Vol. 16, No. 1, pp. 43-49. print.
ISSN: 0767-0974.
DOCUMENT TYPE: Article
LANGUAGE: French
ENTRY DATE: Entered STN: 5 Apr 2000
Last Updated on STN: 3 Jan 2002

AB The Human Genome Project is changing our conception of modern biology. Recent advances in technology are now enabling us to observe complex processes on a genome-wide scale. This review examines the emerging technology of DNA microarrays. Notwithstanding the differences related to manufacture characteristics and properties of the two major technologies used today, DNA microarrays offer the potential to simultaneously investigate thousands of genes. Expression DNA chips containing gene probes rely on the expression profile of collections of genes to investigate complex biochemical pathways, validate drug targets, and classify cell phenotype. Microarrays may be used to detect variations in DNA sequences and correlate these with phenotypes - as in genome scans for linkage studies, mutations detection, large-scale association studies, and analyses of drug responses. Numerous applications related to modern medicine in the areas of diagnostics and drug management are rapidly emerging.

L3 ANSWER 12 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2006:1177492 CAPLUS

DOCUMENT NUMBER: 146:25891
TITLE: Microarray data on gene modulation by HIV-1 in immune cells: 2000-2006
AUTHOR(S): Giri, Malavika S.; Nebozhyn, Michael; Showe, Louise; Montaner, Luis J.
CORPORATE SOURCE: HIV Immunopathogenesis Laboratory, Wistar Institute, Philadelphia, PA, USA
SOURCE: Journal of Leukocyte Biology (2006), 80(5), 1031-1043
CODEN: JLBIE7; ISSN: 0741-5400
PUBLISHER: Federation of American Societies for Experimental Biology
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB Here, we review 34 HIV microarray studies in human immune cells over the period of 2000-March 2006 with emphasis on anal. approaches used and conceptual advances on HIV modulation of target cells (CD4 T cell, macrophage) and nontargets such as NK cell, B cell, and dendritic cell subsets. Results to date address advances on gene modulation associated with immune dysregulation, susceptibility to apoptosis, virus replication, and viral persistence following in vitro or in vivo infection/exposure to HIV-1 virus or HIV-1 accessory proteins. In addition to gene modulation associated with known functional correlates of HIV infection and replication (e.g., T cell apoptosis), microarray data have yielded novel, potential mechanisms of HIV-mediated pathogenesis such as modulation of cholesterol biosynthetic genes in CD4 T cells (relevant to virus replication and infectivity) and modulation of proteasomes and histone deacetylases in chronically infected cell lines (relevant to virus latency). Intrinsic challenges in summarizing gene modulation studies remain in development of sound approaches for comparing data obtained using different platforms and anal. tools, deriving unifying concepts to distil the large vols. of data collected, and the necessity to impose a focus for validation on a small fraction of genes. Notwithstanding these challenges, the field overall continues to demonstrate progress in expanding the pool of target genes validated to date in in vitro and in vivo datasets and understanding the functional correlates of gene modulation to HIV-1 pathogenesis in vivo.
REFERENCE COUNT: 106 THERE ARE 106 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 13 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2006:1128303 CAPLUS
DOCUMENT NUMBER: 145:436595
TITLE: Multiple sclerosis therapy monitoring based on gene expression
AUTHOR(S): Goertsches, Robert; Serrano-Fernandez, Pablo; Moeller, Steffen; Koczan, Dirk; Zettl, Uwe K.
CORPORATE SOURCE: Department of Immunology, University of Rostock, Rostock, 18055, Germany
SOURCE: Current Pharmaceutical Design (2006), 12(29), 3761-3779
CODEN: CPDEFP; ISSN: 1381-6128
PUBLISHER: Bentham Science Publishers Ltd.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Multiple sclerosis (MS) is the most prevalent chronic autoimmune, neurodegenerative disorder of the central nervous system (CNS). Despite substantial progress, treatment of MS and other autoimmune diseases is only moderately effective. It is anticipated that the treatment of autoimmune diseases with single drugs or biol. approaches will in the future be complemented, or even replaced, by combination therapies, which include immunomodulation, elimination of infectious

triggers and tissue repair. One proclaimed goal of biomedical research and clin. practice is the discovery of sets of genes with expression that correlates with successful outcomes of drug therapy, or with unfortunate side effects. Such information has direct consequences for selection, refinement or development of treatments and will soon be translated into clin. trials. The genome-wide RNA profile of an individual represents one complement to the comprehensive determination of disease- or drug response-related elements; comparable to a 'sentinel' method, it serves as a large-scale approach to MS biol. This work reviews the state of the art in MS research at the transcriptome level applying genomewide screening methods. It discusses implications in understanding disease pathogenicity, diagnostic markers, the identification of new therapeutic targets and a classification of patients towards the advent of tailored therapies.

REFERENCE COUNT: 166 THERE ARE 166 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 14 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2006:1112393 CAPLUS

TITLE: Genomics and Proteomics of Bone Cancer

AUTHOR(S): Marguiles, Aaron G.; Klimberg, V. Suzanne; Bhattacharrya, Sudeepa; Gaddy, Dana; Suva, Larry J.

CORPORATE SOURCE: Department of Orthopaedic Surgery, Center for Orthopaedic Research, Barton Research Institute, Department of Surgery, Division of Breast Surgical Oncology, and Department of Physiology and Biophysics, University of Arkansas for Medical Sciences, Little Rock, AR, USA

SOURCE: Clinical Cancer Research (2006), 12(20, Pt. 2), 6217s-6221s
CODEN: CCREF4; ISSN: 1078-0432

PUBLISHER: American Association for Cancer Research

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB Although the control of bone metastasis has been the focus of intensive investigation, relatively little is known about the mol. mechanisms that regulate or predict the process, even though widespread skeletal dissemination is an important step in the progression of many tumors. As a result, understanding the complex interactions contributing to the metastatic behavior of tumor cells is essential for the development of effective therapies. Using a state-of-the-art combination of gene expression profiling and functional annotation of human tumor cells, and surface-enhanced laser desorption/ionization time-of-flight mass spectrometry of patient serum, we have shown that changes in tumor biochem. correlate with disease progression and help to define the aggressive tumor phenotype. Based on these approaches, it is apparent that the metastatic phenotype of tumor cells is extremely complex. The identification of the phenotype of tumor cells has benefited greatly from the application of gene expression profiling (microarray anal.). This technol. has been used by many investigators to identify changes in gene expression and cytokine and growth factor elaboration (such as interleukin 8). The tumor phenotype(s) presumably also include changes in the cell surface carbohydrate profile (via altered glycosyltransferase expression) and heparan sulfate expression (via increased heparanase activity), to name but a few. These specific alterations in gene expression, identified by functional annotation of accumulated microarray data, have been validated using a variety of approaches. Collectively, the data described here suggest that each of these activities is associated with distinct aspects of the aggressive tumor cell phenotype. Collectively, the data suggest that multiple factors constitute the complex phenotype of

metastatic tumor cells. In particular, the differences observed in gene expression profiles and serum protein biomarkers play a critical role in defining the mechanisms responsible for bone-specific colonization and growth of tumors in bone. Future studies will identify the mechanisms that participate in the formation of secondary tumor growths of cancers in bone.

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 15 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2006:1008044 CAPLUS
DOCUMENT NUMBER: 146:225596
TITLE: Gene expression profiling of thyroid tumors- clinical applicability
AUTHOR(S): Lubitz, Carrie C.; Fahey, Thomas J., III
CORPORATE SOURCE: Department of Surgery, Weill Medical College, Cornell University, New York, NY, USA
SOURCE: Nature Clinical Practice Endocrinology & Metabolism (2006), 2(9), 472-473
CODEN: NCPEDB; ISSN: 1745-8366
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Expression genomics has indeed proven a worthy diagnostic and investigative tool. Microarray gene expression profiles were successfully used to discriminate and sub-classify malignant thyroid nodules in ex vivo samples. Differentially expressed genes identified in these expts. are highly accurate at clustering samples with the same morphol. Use of principal component anal. of microarray datasets has shown that there is greater genetic variability between the transcription profiles of samples of different mutational status than between those of different morphol. subtype. Furthermore, categorization of tumors by gene profile is more specific than that by histol. appearance. Mol. profiling could also be important for risk stratification. Although the majority of differentiated thyroid cancers are indolent, up to 10% exhibit an invasive and lethal phenotype. Moreover, BRAF mutations and overexpression of MUC1 are correlated with worse outcomes.

REFERENCE COUNT: 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 16 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2006:274850 CAPLUS
DOCUMENT NUMBER: 145:349073
TITLE: "Promoter array" studies identify cohorts of genes directly regulated by methylation, copy number change, or transcription factor binding in human cancer cells
AUTHOR(S): Wang, Yipeng; Hayakawa, Jun; Long, Fred; Yu, Qiuju; Cho, Ann H.; Rondeau, Gaelle; Welsh, John; Mittal, Shalu; De Belle, Ian; Adamson, Eileen; McClelland, Michael; Mercola, Dan
CORPORATE SOURCE: Sidney Kimmel Cancer Center, San Diego, CA, 92121, USA
SOURCE: Annals of the New York Academy of Sciences (2005), 1058(Therapeutic Oligonucleotides), 162-185
CODEN: ANYAA9; ISSN: 0077-8923
PUBLISHER: New York Academy of Sciences
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. DNA microarrays of promoter sequences have been developed in order to identify the profile of genes bound and activated by DNA regulatory proteins such as the transcription factors

c-Jun and ATF2 as well as DNA-modifying methylases. The arrays contain 3083 unique human promoter sequences from +500 to -1000 nts from the transcription start site. Cisplatin-induced DNA damage rapidly leads to specific activation of the Jun kinase pathway leading to increased phosphorylation of c-Jun and ATF2-DNA complexes at hundreds of sites within 3 h. Using three statistical criteria, approx. 269 most commonly phosphorylated c-Jun/ATF2-DNA complexes were identified and representative cases were verified by qPCR measurement of ChIP-captured DNA. Expression was correlated at the mRNA and protein levels. The largest functional cohort was 24 genes of known DNA repair function, most of which exhibited increased protein expression indicated coordinate gene regulation. In addition, cell lines of prostate cancer exhibit stable methylation or copy number changes that reflect the alterations of the corresponding primary tumors. 504 (18.5%) Promoters showed differential hybridization between immortalized control prostate epithelial and cancer cell lines. Among candidate hypermethylated genes in cancer-derived lines, eight had previously been observed in prostate cancer, and 13 were previously determined methylation targets in other cancers. The vast majority of genes that appear to be both differentially methylated and differentially regulated between prostate epithelial and cancer cell lines are novel methylation targets, including PAK6, RAD50, TLX3, PIR51, MAP2K5, INSR, FBN1, GG2-1, representing a rich new source of candidate genes to study the role of DNA methylation in prostate tumors. Earlier studies using prototype promoter arrays examine approx. 7% of the proximal regulatory sequences while the current gene regulatory events surveyed here occur on a large scale and may rapidly effect the coordinated expression of a large number of genes.

REFERENCE COUNT: 64 THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 17 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2006:137688 CAPLUS
DOCUMENT NUMBER: 144:342940
TITLE: Gene expression profiling for prediction of response to chemotherapy
AUTHOR(S): Shimojo, Takashi; Miki, Yoshio; Nagasaki, Koichi
CORPORATE SOURCE: Cancer Inst., Genome Center, Japanese Foundation for Cancer Res., 3-10-6 Ariake, Koto-ku, Tokyo, 135-8550, Japan
SOURCE: Gan to Kagaku Ryoho (2006), 33(1), 1-5
CODEN: GTKRDX; ISSN: 0385-0684
PUBLISHER: Gan to Kagaku Ryohosha
DOCUMENT TYPE: Journal; General Review
LANGUAGE: Japanese

AB A review. Numerous genes whose expression is controlled by complex regulatory networks are involved in the development and progression of each cancer, and those genes will be the key factors for determining each characteristic of the tumor. The recent development of DNA microarray and related technologies provides an opportunity to perform more detailed characterization (profiling) of individual tumor cells. Indeed, the gene expression profile of a tumor provides a unique mol. portrait or signature that can be correlated with clin. behavior and drug responsiveness. The development of personalized (or customized) medicine and molecularly targeted drugs is enthusiastically awaited based on the results of research examining genomic diversity such as SNPs (single nucleotide polymorphisms), gene expression profiling with DNA microarrays, and anal. of protein expression and interactions.

L3 ANSWER 18 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2006:22226 CAPLUS
DOCUMENT NUMBER: 145:205228
TITLE: Microarray-based functional protein profiling using peptide nucleic acid-encoded libraries
AUTHOR(S): Winssinger, Nicolas; Harris, Jennifer L.
CORPORATE SOURCE: Institut de Science et Ingenierie Supramoleculaires, Organic & Bioorganic Chemistry Laboratory, Universite Louis Pasteur, Strasbourg, 67000, Fr.
SOURCE: Expert Review of Proteomics (2005), 2(6), 937-947
CODEN: ERPXA3; ISSN: 1478-9450
PUBLISHER: Future Drugs Ltd.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. The availability of complete genome sequences from numerous organisms has provided investigators with the challenge of assigning physiol. functions to the encoded gene products. To facilitate this process, multiple technologies have been developed to profile the transcriptome and the proteome, including methods to monitor the function of enzymes in complex biol. systems. These methods typically target specific classes of enzymes and attempt to correlate the enzymic activity with the specific phenotype of interest. Here, technologies to measure enzymic activity on a subproteomic scale are reviewed, including the authors' own efforts, which are based on self-assembled microarrays utilizing peptide nucleic acid-encoded small-mol. libraries.
REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 19 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:1292921 CAPLUS
DOCUMENT NUMBER: 144:251217
TITLE: Melanocyte and keratinocyte carcinogenesis: p53 family protein activities and intersecting mRNA expression profiles
AUTHOR(S): Kulesz-Martin, Molly; Lagowski, James; Fei, Suzanne; Pelz, Carl; Sears, Rosalie; Powell, Marianne Broome; Halaban, Ruth; Johnson, Jodi
CORPORATE SOURCE: Department of Dermatology, Oregon Health and Science University, Portland, OR, USA
SOURCE: Journal of Investigative Dermatology Symposium Proceedings (2005), 10(2), 142-152
CODEN: JDSPFO; ISSN: 1087-0024
PUBLISHER: Blackwell Publishing, Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Melanocytes and keratinocytes were analyzed for potential roles of p53, p73, and p63 tumor suppressor family proteins and of malignancy-specific gene expression changes in the etiol. of multi-step cancer. Melanocytes expressed ΔNp73α, two p63 isoforms and p53. Although p21 and Noxa mRNA levels increased following DNA damage, p53 family member binding to p21 and Noxa DNA probes was undetectable, suggesting p53 family-independent responses. In contrast, keratinocytes expressed multiple isoforms each of p73 and p63 that were induced to bind p21 and Noxa DNA probes after ionizing (IR) or after UV B (UVB) irradiation, correlating with p21 and Noxa mRNA induction and with apoptosis. Interestingly, IR-resistant malignant melanocytes and keratinocytes both exhibited Noxa mRNA induction after UVB treatment, correlating with DNA binding of p53 family proteins to the Noxa probe only in keratinocytes. To uncover other malignancy-specific events, we queried mouse initiated keratinocyte clones for early changes that were exacerbated in malignant derivs. and also differentially expressed in human advanced melanoma vs. normal melanocytes. Using a new method for

ranking and normalization of microarray data for 5000 probe sets, 27 upregulated and 13 downregulated genes satisfied our query. Of these, the majority was associated with late-stage human cancers and six were novel genes. Thus, clonal lineage mouse models representing early through late cancer progression stages may inform the focus on early, potentially causal events from microarray studies of human cancers, facilitating prognosis and mol. therapy.

REFERENCE COUNT: 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 20 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:1254945 CAPLUS
DOCUMENT NUMBER: 144:267348
TITLE: Estrogen signaling and prediction of endocrine therapy
AUTHOR(S): Hayashi, Shin-Ichi; Yamaguchi, Yuri
CORPORATE SOURCE: Department of Medical Technology, School of Medicine, Course of Health Sciences, Tohoku University, 2-1 Seiryou-machi, Aoba-ku, Sendai, 980-8575, Japan
SOURCE: Cancer Chemotherapy and Pharmacology (2005), 56(Suppl. 1), s27-s31
CODEN: CCPHDZ; ISSN: 0344-5704
PUBLISHER: Springer
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. Estrogen plays an important role in the growth and progression of human breast cancer. A review. Understanding the whole picture of estrogen signaling is a very important goal towards clarifying the biol. of this disease. On the other hand, hormonal therapy for breast cancer has been progressing rapidly with the advent of drugs such as selective estrogen receptor (ER) modulators and aromatase inhibitors. Prediction of individual response to these hormonal therapies is becoming important for the management of breast cancer patients. To help address these basic and clin. issues, we are developing several new tools such as the focused microarray and the green fluorescent protein-reporter cell system. We first carried out expression profiling of approx. 10,000 genes in ER-pos. breast cancer cells. Based on the results, estrogen-responsive genes (ERG) were selected and a custom-made cDNA microarray consisting of 200 genes from a narrowed-down subset was produced. Using this microarray, we investigated various aspects of estrogen signaling such as the effect of estrogen-antagonists on ERG expression profile and functional anal. of ERβ and novel estrogen responsive gene EGR3. Furthermore, expression levels of several candidate genes selected from the custom-array contents were analyzed by real-time RT-PCR and immunohistochem. using breast cancer tissues to determine novel predictive factors for responsiveness to hormone therapy in primary breast cancer patients. Expression of several genes, such as HDAC6, significantly correlated with disease-free and overall survival of patients treated with adjuvant tamoxifen therapy. We are currently developing a new tool for analyzing the effects of novel aromatase inhibitors in individual breast cancer patients using estrogen-responsive element-green fluorescent protein-indicator cells. We hope that these approaches may provide not only new clues for elucidation of estrogen-dependent growth mechanisms of cancer, but also clin. benefits to patients by assessment of individual responses to endocrine therapy.

REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 21 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:1225762 CAPLUS
DOCUMENT NUMBER: 144:209726
TITLE: The results of the expression array studies correlate and enhance the known

genetic basis of gastric and colorectal cancer
AUTHOR(S): Galamb, Orsolya; Sipos, Ferenc; Fischer, Krisztina; Tulassay, Zsolt; Molnar, Bela
CORPORATE SOURCE: II Department of Medicine, Faculty of Medicine Budapest, Semmelweis University, Hung.
SOURCE: Cytometry, Part B: Clinical Cytometry (2005), 68B(1), 1-17
CODEN: CPBCB5; ISSN: 1552-4949
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Gastric and colorectal cancers belong to the most frequent cancer types in the world today. This fact emphasizes the importance of identification of useful diagnostic and prognostic markers, in the earliest stage of the disease. The examination of gene expression profile in gastric and colorectal cancer may develop the bases of early diagnosis and of individual therapeutic strategies. In the microarray examns. done so far for these types of cancers, the expression of hundreds and thousands of genes were studied, however, both the sample collection and the results showed wide variations. The diversity of expression array methods and data anal. makes the comparison of microarray results difficult. Beside the exposition of the practical aspects of the chip technol., our aims are the systematization of data that are currently available in the international scientific literature and the description of the results in a comprehensive way. Microarray results show that the gene expression pattern, detected in gastric and colon cancers, highly depends on the histol. type and heterogeneity of the sample, array type, and softwares, used for data anal. Recent expts. point out not just the changes of the alterations of tumor suppression, apoptosis, cell-cycle regulation, and signal transduction, but tumor cell metabolism and cell-microenvironment interactions also. Results show connection to and make more complete the already known mol. background of gastric and colorectal cancers. Based on the accumulation of recent and further data, such kind of multifunctional diagnostic microarrays that can be suited for completing the conventional histol. diagnostics and subtypization will certainly become available in the near future.
REFERENCE COUNT: 80 THERE ARE 80 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 22 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:1215213 CAPLUS
DOCUMENT NUMBER: 144:461309
TITLE: From microarray to biological networks: Analysis of gene expression profiles
AUTHOR(S): Wu, Xiwei; Dewey, T. Gregory
CORPORATE SOURCE: Keck Graduate Institute of Applied Life Sciences, Claremont, CA, USA
SOURCE: Methods in Molecular Biology (Totowa, NJ, United States) (2005), 316, 35-48
CODEN: MMBIED; ISSN: 1064-3745
PUBLISHER: Humana Press Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Powerful new methods, such as expression profiles using cDNA arrays, have been used to monitor changes in gene expression levels as a result of a variety of metabolic, xenobiotic, or pathogenic challenges. This potentially vast quantity of data enables, in principle, the dissection of the complex genetic networks that control the patterns and rhythms of gene expression in the cell. Here we present a general approach to

developing dynamic models for analyzing time series of whole-genome expression. The parameters in the model show the influence of one gene expression level on another and are calculated using singular value decomposition as a means of inverting noisy and near-singular matrixes. Correlative networks can then be generated based on these parameters with a simple threshold approach. We also demonstrate how dynamic models can be used in conjunction with cluster anal. to analyze microarray time series. Using the parameters from the dynamic model as a metric, two-way hierarchical clustering could be performed to visualize how influencing genes affect the expression levels of responding genes. Application of these approaches is demonstrated using gene expression data in yeast cell cycle.

REFERENCE COUNT: 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 23 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:1107574 CAPLUS

DOCUMENT NUMBER: 144:382494

TITLE: Genomic medicine: genetic variation and its impact on the future of health care

AUTHOR(S): Willard, Huntington F.; Angrist, Misha; Ginsburg, Geoffrey S.

CORPORATE SOURCE: Institute for Genome Sciences & Policy, CIEMAS 2376, Duke University, Durham, NC, 27708, USA

SOURCE: Philosophical Transactions of the Royal Society of London, Series B: Biological Sciences (2005), 360(1460), 1543-1550
CODEN: PTRBAE; ISSN: 0962-8436

PUBLISHER: Royal Society

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review. Advances in genome technol. and other fruits of the Human Genome Project are playing a growing role in the delivery of health care. With the development of new technologies and opportunities for large-scale anal. of the genome, transcriptome, proteome and metabolome, the genome sciences are poised to have a profound impact on clin. medicine. Cancer prognostics will be among the first major test cases for a genomic medicine paradigm, given that all cancer is caused by genomic instability, and microarrays allow assessment of patients' entire expressed genomes. Anal. of breast cancer patients' expression patterns can already be highly correlated with recurrence risks. By integrating clin. data with gene expression profiles, imaging, metabolomic profiles and proteomic data, the prospect for developing truly individualized care becomes ever more real. Notwithstanding these promises, daunting challenges remain for genomic medicine. Success will require planning robust prospective trials, analyzing health care economic and outcome data, assuaging insurance and privacy concerns, developing health delivery models that are com. viable and scaling up to meet die needs of the whole population.

REFERENCE COUNT: 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 24 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:690509 CAPLUS

DOCUMENT NUMBER: 143:343395

TITLE: The importance of colonic butyrate transport to the regulation of genes associated with colonic tissue homeostasis

AUTHOR(S): Daly, K.; Cuff, M. A.; Fung, F.; Shirazi-Beechey, S. P.

CORPORATE SOURCE: Epithelial Function and Development Group, Department of Veterinary Preclinical Sciences, University of

Liverpool, Liverpool, L69 7ZJ, UK
SOURCE: Biochemical Society Transactions (2005), 33(4), 733-735
CODEN: BCSTB5; ISSN: 0300-5127
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. The transition from normality to malignancy in colorectal cancer is characterized by alterations in the expression of genes associated with the maintenance of tissue homeostasis. Butyrate, a product of microbial fermentation of dietary fiber in the colon, is known to regulate a number of genes associated with the processes of proliferation, differentiation, and apoptosis of colonic epithelial cells, and, hence, homeostasis of colonic tissue. We have shown previously that the transport of butyrate into colonocytes is of fundamental importance to butyrate's regulatory ability, and therefore sought to assess the expression profile of butyrate-responsive genes in colon cancer tissue, where the expression of the colonic luminal-membrane butyrate transporter, MCT1 (monocarboxylate transporter 1), is significantly down-regulated. In the present paper, we first employed microarray anal. to assess global changes in butyrate-responsive genes using HT29 human colon carcinoma cells treated with butyrate. There was consistency in the butyrate response of selected genes in 2 other human colonic cell lines (HCT116 and AA/C1) using quant. real-time PCR. Furthermore, we report that expression levels of selected butyrate-responsive genes involved in the processes of proliferation, differentiation and apoptosis, are deregulated in colon cancer tissue, correlating with decreased expression of MCT1. These findings support our hypothesis that a reduction in MCT1 expression, and hence butyrate transport, can lead to a reduction in the intracellular butyrate levels required to regulate gene expression. Collectively, our results highlight the important contribution of butyrate transport to the maintenance of tissue homeostasis and disease prevention.
REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 25 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:311184 CAPLUS
DOCUMENT NUMBER: 143:112989
TITLE: Gene expression pattern of obese and control individuals in adipose tissue and peripheral blood mononuclear cells
AUTHOR(S): Garcia-Amigot, F.; Lamas, O.; Marti, A.; Aliaga, M. J. Moreno; Bandres, E.; Garcia-Foncillas, J.; Martinez, J. A.
CORPORATE SOURCE: Department of Physiology and Nutrition, Department of Oncology, University of Navarra, Pamplona, 31008, Spain
SOURCE: Trends in Obesity Research (2005), 67-84. Editor(s): Ling, Peter R. Nova Science Publishers, Inc.: Hauppauge, N. Y.
CODEN: 69GSY9; ISBN: 1-59454-142-6
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review. Obesity is a serious and growing public health problem throughout the world. Increased food intake and decreased energy expenditure due to sedentary lifestyles in modem societies have contributed to the widespread development of obesity. Moreover, the genetic background is a key factor for different diseases such as diabetes mellitus, hypertension, cancer, obesity, etc. In this context, different genes are involved in the body weight and fat mass maintenance, through their role in the control of afferent mechanisms (leptin, nutrients, nervous

signals...), central mechanisms (hypothalamic neurotransmisors) and efferent mechanisms (insulin, catecholamines...). So, energy balance and body composition seems to depend up to a 40% of the genetic background. Several investigations using different approaches and protocols have identified more than 430 genes and genetic markers involved in the onset and development of obesity. In this context, we analyzed by a microarray technol. the gene expression pattern of obese and control individuals in adipose tissue and peripheral blood mononuclear cells (PBMCs). This approach found 129 genes up-regulated and 1009 genes down-regulated in adipose tissue from control subjects when compared to obese individuals and 15 genes up-regulated and 201 genes down-regulated in lymphocytes of controls compared to obese individuals. These results have been confirmed by real time PCRs on three selected genes (cab45, adrala, mgc4365). Finally, the data obtained from adipose tissue and PBMCs were conjointly assessed and 35 genes down-regulated both in adipose tissue and lymphocytes from controls compared to obese were found. However, when the profiles of gene expression by quant. PCRs in adipose tissue and lymphocytes were analyzed, only the adipose tissue pattern of gene expression correlated well concerning the microarray validation. Moreover, there was no association in the pattern of gene expression in lymphocytes between the data obtained by microarray and by quant. PCRs. Summing up, it has been shown that obesity not only affects the pattern of gene expression in adipose tissue, but also the pattern of gene expression in immune system cells, although these patterns do not correlate apparently much between them.

REFERENCE COUNT: 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 26 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:95091 CAPLUS
DOCUMENT NUMBER: 143:1727
TITLE: Artificial neural network technologies to identify biomarkers for therapeutic intervention
AUTHOR(S): Bicciato, Silvio
CORPORATE SOURCE: Department of Chemical Engineering Processes, University of Padova, Padua, 35131, Italy
SOURCE: Current Opinion in Molecular Therapeutics (2004), 6(6), 616-623
CODEN: CUOTFO; ISSN: 1464-8431
PUBLISHER: Thomson Scientific
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. High-throughput technologies such as DNA/RNA microarrays, mass spectrometry and protein chips are creating unprecedented opportunities to accelerate towards the understanding of living system and the identification of target genes and pathways for drug development and therapeutic intervention. However, the increasing vols. of data generated by mol. profiling expts. pose formidable challenges to investigate an overwhelming mass of information and turn it into predictive, deployable markers. Advanced biostatistics and machine learning methods from computer science have been applied to analyze and correlate numerical values of profiling intensities to physiol. states. This article reviews the application of artificial neural networks, an information-processing tool, to the identification of sets of diagnostic/prognostic biomarkers from high-throughput profiling data.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 27 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2004:1123435 CAPLUS
DOCUMENT NUMBER: 142:258608

TITLE: Analysis of gastric cancer with cDNA microarray
AUTHOR(S): Haraguchi, Naotsugu; Inoue, Hiroshi; Mimori, Koshi; Tanaka, Fumiaki; Utsunomiya, Tohru; Yoshikawa, Kouji; Mori, Masaki
CORPORATE SOURCE: Department of Surgery and Molecular Oncology, Medical Institute of Bioregulation, Kyushu University, Beppu, 874-0838, Japan
SOURCE: Cancer Chemotherapy and Pharmacology (2004), 54(Suppl. 1), S21-S24
CODEN: CCPHDZ; ISSN: 0344-5704
PUBLISHER: Springer GmbH
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review on the pros and cons for cDNA microarray anal. in the context of gastric cancer. Recent advances in cDNA microarray techniques have enabled the study of the expression of many genes simultaneously. As gastric cancer remains one of the most common cancers in Japan, the authors studied gene expression profiles in gastric cancer by cDNA microarray anal. to determine if it would be clin. useful. The authors demonstrated two points. First, cDNA microarray might be useful as a prognostic indicator. However, there remain several important problems to be solved and these are discussed. Second, laser microdissection plus cDNA microarray might be useful in determining the specific genes that correlate to cancer metastasis or histol. subtype.
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 28 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2004:975177 CAPLUS
DOCUMENT NUMBER: 142:255222
TITLE: What do microarrays really tell us about M. tuberculosis?
AUTHOR(S): Kendall, Sharon L.; Rison, Stuart C. G.; Movahedzadeh, Farahnaz; Frita, Rosangela; Stoker, Neil G.
CORPORATE SOURCE: Department of Pathology and Infectious Diseases, Royal Veterinary College, London, NW1 0TU, UK
SOURCE: Trends in Microbiology (2004), 12(12), 537-544
CODEN: TRMIEA; ISSN: 0966-842X
PUBLISHER: Elsevier Ltd.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Bacterial pathogens adapt to their host environments to a large extent through switching on complex transcriptional programs, and whole-genome microarray expts. promise to reveal this complexity. There has been a recent burst of articles reporting transcriptome analyses of Mycobacterium tuberculosis, including for the first time studies in macrophages and mice. Authors review gene expression reports, and compare them with each other and with microarray-based gene essentiality studies, revealing at times a startling lack of correlation. Addnl., authors suggest a standardization format for the submission of processed data for publication, to facilitate cross-experiment analyses.
REFERENCE COUNT: 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 29 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2004:394115 CAPLUS
DOCUMENT NUMBER: 141:34317
TITLE: A comparison of global gene expression measurement technologies in

Arabidopsis thaliana
AUTHOR(S): Coughlan, Sean J.; Agrawal, Vikas; Meyers, Blake
CORPORATE SOURCE: Agilent Technologies Inc., Wilmington, DE, 19808-1644, USA
SOURCE: Comparative and Functional Genomics (2004), 5(3), 245-252
CODEN: CFGOAT; ISSN: 1531-6912
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Microarrays and tag-based transcriptional profiling technologies represent diverse but complementary data types. A comparison of high-d. in situ synthesized microarrays and massively-parallel signature sequencing (MPSS) data in the model plant, Arabidopsis thaliana was conducted. The MPSS data (available at http://mpss.udel.edu/at) and the microarray data have been compiled using the same RNA source material. In this review, the exptl. strategy was described, and present preliminary data and interpretations from the transcriptional profiles of Arabidopsis leaves and roots. The preliminary data indicate that the log ratio differences of transcripts between leaves and roots measured by microarray data are in better agreement with the MPSS data than the absolute intensities measured for individual microarrays hybridized to only one of the cRNA populations. The correlation was substantially improved by focusing on a subset of genes excluding those with very low expression levels; this selection may have removed noisy data. Future reports will incorporate more than 10 tissues that have been sampled by MPSS.
REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 30 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2004:111234 CAPLUS
DOCUMENT NUMBER: 140:369382
TITLE: Effect of agonal and postmortem factors on gene expression profile: quality control in microarray analyses of postmortem human brain
AUTHOR(S): Tomita, Hiroaki; Vawter, Marquis P.; Walsh, David M.; Evans, Simon J.; Choudary, Prabhakara V.; Li, Jun; Overman, Kevin M.; Atz, Mary E.; Myers, Richard M.; Jones, Edward G.; Watson, Stanley J.; Akil, Huda; Bunney, William E.
CORPORATE SOURCE: Department of Psychiatry and Human Behavior, University of California, Irvine, Irvine, CA, USA
SOURCE: Biological Psychiatry (2004), 55(4), 346-352
CODEN: BIPCBF; ISSN: 0006-3223
PUBLISHER: Elsevier Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. There are major concerns that specific agonal conditions, including coma and hypoxia, might affect RNA (RNA) integrity in postmortem brain studies. It was shown that agonal factors significantly affect RNA integrity and have a major impact on gene expression profiles in microarrays. In contrast to agonal factors, gender, age, and postmortem factors have less effect on gene expression profiles. The Average Correlation Index is proposed as a method for evaluating RNA integrity on the basis of similarity of microarray profiles. Reducing the variance due to agonal factors is critical in investigating small but validated gene expression differences in mRNA levels between psychiatric patients and control subjects.
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 31 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2004:47549 CAPLUS
DOCUMENT NUMBER: 140:214944
TITLE: Gene expression profiling in childhood acute leukemia: progress and perspectives
AUTHOR(S): Hayashi, Yasuhide
CORPORATE SOURCE: Gunma Children's Medical Center, Gunma, 377-8577, Japan
SOURCE: International Journal of Hematology (2003), 78(5), 414-420
CODEN: IJHEEY; ISSN: 0925-5710
PUBLISHER: Carden Jennings Publishing
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Recent advances in treatment have transformed childhood acute leukemias into curable diseases. However, 20% to 40% of acute leukemia patients still experience a relapse. Microarrays typically contain thousands of oligonucleotides or complementary DNAs and are rapidly becoming important research tools for the identification of novel classifications of leukemias and lymphomas. Microarray-based identification of several translocations has been performed in acute lymphoblastic leukemia (ALL), leading to the discovery of t(1;19), t(12;21), and 11q23 translocations, and in acute myeloid leukemia (AML), finding t(8;21), inv(16), and t(15;17). Correlations between gene expression profiles and clin. features have been reported in ALL and AML. Recently, it was reported that gene expression profiling can be used to predict the prognosis of childhood acute leukemia. In this report, the recent progress in microarray anal. of childhood acute leukemia is reviewed. Gene expression profiling provides new insights into the biol. mechanisms of leukemogenesis and the prognosis of childhood acute leukemia.
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 32 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2003:161212 CAPLUS
DOCUMENT NUMBER: 138:351829
TITLE: Understanding cancer through gene expression profiling
AUTHOR(S): Aburatani, Hiroyuki
CORPORATE SOURCE: Genome Science Division, Research Center for Advanced Science and Technology, The University of Tokyo, Meguro-ku, Tokyo, 153-8904, Japan
SOURCE: International Congress Series (2002), 1246(Genome Science: Towards a New Paradigm?), 261-270
CODEN: EXMDA4; ISSN: 0531-5131
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Various genomic technologies have been applied to address crucial problems in cancer biol., as cancer is caused through the accumulation of various genetic alterations. Among all, transcriptome anal. using microarray will be expected to identify novel mol. targets for therapeutics and/or diagnostics of cancer, which expression levels are often dys-regulated in cancer tissues. We applied high-d. oligonucleotide array anal. to monitor gene expression in tumors and non-tumor tissues. Correlation of expression profile data with clinico-pathol. parameters was analyzed, then classifier genes were selected when pos. correlation was observed Furthermore, as integration of transcriptome information with other biol. data is crucial

to interpret microarray data, we developed a graphical presentation tool, 'expression imbalance map', which displays gene expression data along with chromosomal positions. Such anal. results were not only comparable with allelic imbalance data reported previously and also at a single gene resolution Genes which were identified to be highly expressed in tumor tissues would be good candidates for mol. therapeutics or diagnostics, especially when they are either membrane-associated or secreted mols., resp. We have recently analyzed expression levels of over 20,000 genes in 40 different human tissues. Those data are freely available to the public through our gene expression database, SMB-DB (Systems Biol. and Medicine Database), and will be also utilized to obtain the tissue distribution profiles for such candidate genes.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 33 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2003:39995 CAPLUS

DOCUMENT NUMBER: 138:302670

TITLE: Mapping stresses in Escherichia coli to improve yield

AUTHOR(S): DeLisa, Matthew P.; Gill, Ryan T.; Bentley, William E.

CORPORATE SOURCE: Cent. for Agric. Biotechnol., Univ. of Maryland Biotechnol. Inst., College Park, MD, USA

SOURCE: Recombinant Protein Production with Prokaryotic and Eukaryotic Cells: A Comparative View on Host Physiology, Selected Articles from the Meeting of the EFB Section on Microbial Physiology, Semmering, Austria, Oct. 5-8, 2000 (2001), Meeting Date 2000, 43-54. Editor(s): Merten, Otto-Wilhelm. Kluwer Academic Publishers: Dordrecht, Neth.
CODEN: 69DLJQ; ISBN: 0-7923-7137-2

DOCUMENT TYPE: Conference; General Review

LANGUAGE: English

AB A review. The specific yield of recombinant E. coli has for many years and for many proteins decreased with increased cell d. New anal. techniques are becoming available that will facilitate a detailed understanding of this phenomena. RTPCR amplified mRNA from induced and control cells were hybridized with a DNA array of Kohara clones representing 16% (700 genes) of the E. coli genome. Subsequently, Northern anal. was performed for quantification of specific gene dynamics and statistically significant overlap in the regulation of 11 stress related genes was found using correlation anal. The results reported here establish, for the first time, that there are dramatic changes in the transcription rates of a broad range of stress genes (representing multiple regulons) after induction of recombinant protein, in general, and that differences in these changes can, in part, be explained by features of the recombinant protein. Further, it was found that transcriptional regulation of stress-related genes in E. coli at high cell d. is profoundly different than at low cell d. Specifically, RTPCR amplified mRNA from low (4 g DCW/L) and high-cell-d. (43.5 g DCW/L) conditions were hybridized with a DNA microarray encompassing 16% of the E. coli genome and differentially displayed genes were identified. Subsequently, transcript specific RNA dot blots indicated that mol. chaperones (groEL, ibpA, degP), proteases (degP, ftsH), the lysis gene mltB; and DNA damage/bacteriophage associated gene transcript levels (ftsH, recA, alpA, uvrB) increased 10-43 fold at high cell d. Importantly, we will discuss these phenomena, as well as "cell conditioning" strategies to exploit our understanding of stress responses in E. coli in order to increase yield.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 34 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2002:942358 CAPLUS
DOCUMENT NUMBER: 138:215393
TITLE: Glucose-regulated gene expression maintaining the glucose-responsive state of β-cells
AUTHOR(S): Schuit, Frans; Flamez, Daisy; De Vos, Anick; Pipeleers, Daniel
CORPORATE SOURCE: Diabetes Research Center, Faculty of Medicine, Vrije Universiteit Brussel, Brussels, B-1090, Belg.
SOURCE: Diabetes (2002), 51(Suppl. 3), S326-S332
CODEN: DIAEAZ; ISSN: 0012-1797
PUBLISHER: American Diabetes Association
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. The mammalian β-cell has particular properties that synthesize, store, and secrete insulin in quantities that are matched to the physiol. demands of the organism. To achieve this task, β-cells are regulated both acutely and chronically by the extracellular glucose concentration Several in vivo and in vitro studies indicate that preservation of the glucose-responsive state of β-cells is lost when the extracellular glucose concentration chronically deviates from the normal physiol. condition. Expts. with the protein synthesis inhibitor cycloheximide suggest that the maintenance of the functional state of β-cells depends on protein(s) with rapid turnover. Anal. of newly synthesized proteins via two-dimensional gel electrophoresis and high-d. gene expression microarrays demonstrates that the glucose-dependent preservation of β-cell function is correlated with glucose regulation of a large number of β-cell genes. Two different microarray analyses of glucose regulation of the mRNA profile in β-cells show that the sugar influences expression of multiple genes involved in energy metabolism, the regulated insulin biosynthetic/secretory pathway, membrane transport, intracellular signaling, gene transcription, and protein synthesis/degradation Functional anal. of some of these regulated gene clusters has provided new evidence for the concept that cataplerosis, the conversion of mitochondrial metabolites into lipid intermediates, is a major metabolic pathway that allows β-cell activation independently of closure of ATP-sensitive potassium channels.

REFERENCE COUNT: 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 35 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2002:17214 CAPLUS
DOCUMENT NUMBER: 137:104188
TITLE: Gene expression profiles for monitoring radiation exposure
AUTHOR(S): Amundson, S. A.; Fornace, A. J., Jr.
CORPORATE SOURCE: National Cancer Institute Division of Basic Science, National Institutes of Health, Bethesda, MD, 20892, USA
SOURCE: Radiation Protection Dosimetry (2001), 97(1), 11-16
CODEN: RPDODE; ISSN: 0144-8420
PUBLISHER: Nuclear Technology Publishing
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with refs. Previous demonstrations that the dose, dose rate, radiation quality, and elapsed time since ionizing radiation exposure result in variations in the response of stress genes suggest that gene expression signatures may be informative markers of radiation exposure. Defining sets of genes that are specific for different outcomes of interest will be key to such an approach. A generalized post-exposure profile may identify exposed individuals within a population, while more specific fingerprints may

reveal details of a radiation exposure. Changes in gene expression in human cell lines occur after as little as 0.02 Gy γ rays, and in peripheral blood lymphocytes after as little as 0.2 Gy. Diverse genes are also elevated in vivo in mice 24 h after 0.2 Gy irradiation Ongoing microarray analyses meanwhile continue to identify large nos. of potential biomarkers from varied irradiation protocols. Development of computation-intensive informatics anal. methods will be needed for management of the complex gene expression profiles resulting from such expts. Although the preliminary data are encouraging, significant work remains before meaningful correlations with risk or practical assessment of exposure can be made by gene expression profiling.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 36 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2001:393147 CAPLUS

DOCUMENT NUMBER: 136:97859

TITLE: Protein microarrays - a tool for the post-genomic era

AUTHOR(S): Lueking, Angelika; Konthur, Zoltan; Eickhoff, Holger; Bussow, Konrad; Lehrach, Hans; Cahill, Dolores J.

CORPORATE SOURCE: Max Planck Institute of Molecular Genetics, Berlin, D-14195, Germany

SOURCE: Current Genomics (2001), 2(2), 151-159
CODEN: CGUEA8; ISSN: 1389-2029

PUBLISHER: Bentham Science Publishers Ltd.

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review. The human genome is sequenced and the challenges of understanding the function of the newly discovered genes have been addressed. For this purpose, high-throughput technologies have been developed that allow the monitoring of gene activity at the transcriptional level by anal. of complex expression patterns of a specific tissue. Differential gene expression can be most efficiently monitored by oligonucleotide or cDNA hybridization on DNA arrays. Recently, protein arrays are emerging to follow DNA chips as a tool to profile protein products encoded by globally or differentially expressed cDNA clones. Array technol. was enabled by the development of devices that could array biol. samples at high d. with high precision onto immobilizing surfaces, ranging from the classic microtiter plate to new chip-sized supports. In addition, the introduction of automated technol. to the protein level involves the simultaneous expression of a large number of cDNA clones in an appropriate vector and expression system, allowing the specific detection and purification of all the recombinant proteins. With the ordered arrangement of recombinantly expressed proteins, a direct link to the corresponding DNA sequence information is possible and consequently, clone libraries become amenable to be integrated in a database including all steps from DNA sequencing to functional assays of the translated gene product. Here, we review the generation and application of microarray technol. as a highly parallel approach to obtain more information on the regulation of proteins, their biochem. function and potential interaction partners. Already, a large variety of assays based on antibody-antigen interaction exists and in addition, the medical relevance of protein arrays will be discussed. Also, further applications such as protein-DNA, protein-RNA and protein-substrate interactions will be presented, since initial studies on immobilized proteins were reported. Proteomics is an emerging field to profile protein repertoires. Because there is no reliable correlation between gene activity monitored by genomic studies and cellular protein abundance, application of protein arrays will link both genomics and proteomics.

REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 37 OF 47 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2006:14531 SCISEARCH
THE GENUINE ARTICLE: 995KM
TITLE: Harnessing the power of gene microarrays for the study of brain aging and Alzheimer's disease: Statistical reliability and functional correlation
AUTHOR: Blalock E M (Reprint); Chen K C; Stromberg A J; Norris C M; Kadish I; Kraner S D; Porter N M; Landfield P W
CORPORATE SOURCE: Univ Kentucky, Med Ctr, Dept Mol & Biomed Pharmacol, 800 Rose St MS 309, Lexington, KY 40536 USA (Reprint); Univ Kentucky, Med Ctr, Dept Mol & Biomed Pharmacol, Lexington, KY 40536 USA; Univ Kentucky, Dept Stat, Lexington, KY 40536 USA; Univ Kentucky, Sanders Brown Ctr Aging, Lexington, KY USA; Univ Alabama, Dept Cell Biol, Birmingham, AL 35294 USA
emblal@uky.edu
COUNTRY OF AUTHOR: USA
SOURCE: AGEING RESEARCH REVIEWS, (NOV 2005) Vol. 4, No. 4, pp. 481-512.
ISSN: 1568-1637.
PUBLISHER: ELSEVIER IRELAND LTD, ELSEVIER HOUSE, BROOKVALE PLAZA, EAST PARK SHANNON, CO, CLARE, 00000, IRELAND.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 84
ENTRY DATE: Entered STN: 11 Jan 2006
Last Updated on STN: 11 Jan 2006

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB During normal brain aging, numerous alterations develop in the physiology, biochemistry and structure of neurons and glia. Aging changes occur in most brain regions and, in the hippocampus, have been linked to declining cognitive performance in both humans and animals. Age-related changes in hippocampal regions also may be harbingers of more severe decrements to come from neurodegenerative disorders such as Alzheimer's disease (AD). However, unraveling the mechanisms underlying brain aging, AD and impaired function has been difficult because of the complexity of the networks that drive these aging-related changes. Gene microarray technology allows massively parallel analysis of most genes expressed in a tissue, and therefore is an important new research tool that potentially can provide the investigative power needed to address the complexity of brain aging/ neurodegenerative processes. However, along with this new analytic power, microarrays bring several major bioinformatics and resource problems that frequently hinder the optimal application of this technology. In particular, microarray analyses generate extremely large and unwieldy data sets and are subject to high false positive and false negative rates. Concerns also have been raised regarding their accuracy and uniformity, Furthermore, microarray analyses can result in long lists of altered genes, most of which may be difficult to evaluate for functional relevance. These and other problems have led to some skepticism regarding the reliability and functional usefulness of microarray data and to a general view that microarray data should be validated by an independent method. Given recent progress, however, we suggest that the major problem for current microarray research is no longer validity of expression measurements, but rather, the reliability of inferences from the data, an issue more appropriately redressed by statistical approaches than by validation with a separate method. If tested using statistically defined criteria for reliability/significance, microarray data do not appear a priori to require more independent validation than data obtained by any other method. In fact, because of

added confidence from co-regulation, they may require less. In this article we also discuss our strategy of statistically correlating individual gene expression with biologically important endpoints designed to address the problem of evaluating functional relevance. We also review how work by ourselves and others with this powerful technology is leading to new insights into the complex processes of brain aging and AD, and to novel, more comprehensive models of aging-related brain change. (c) 2005 Elsevier Ireland Ltd. All rights reserved.

L3 ANSWER 38 OF 47 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 2007054960 EMBASE
TITLE: Gene expression profile assays as predictors of recurrence-free survival in early-stage breast cancer: A metaanalysis.
AUTHOR: Lyman G.H.; Kuderer N.M.
CORPORATE SOURCE: Dr. G.H. Lyman, University of Rochester School of Medicine and Dentistry, James P. Wilmot Cancer Center, University of Rochester Medical Center - Strong Memorial Hospital, 601 Elmwood Ave, Box 704, Rochester, NY 14642, United States. gary_lyman@urmc.rochester.edu
SOURCE: Clinical Breast Cancer, (2006) Vol. 7, No. 5, pp. 372-379.
Refs: 35
ISSN: 1526-8209 CODEN: CBCLB7
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
022 Human Genetics
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 28 Feb 2007
Last Updated on STN: 28 Feb 2007

AB Background: Several investigators have reported efforts to define gene expression signatures based on prediction of survival in early-stage breast cancer. The analysis reported here reviews test performance characteristics of reported gene expression signatures in women with breast cancer. Patients and Methods: All published reports of gene expression profiling in breast cancer were sought through an extensive search of the published literature. Seventeen cohorts of patients with primary breast cancer were identified reporting on the relationship between a gene expression signature and recurrence-free survival. Several measures of test performance were evaluated including sensitivity, specificity, likelihood ratio, predictive value, and the diagnostic odds ratio as an overall measure of test performance. Results: Reported series included 2908 patients ranging from 20 to 668 per study. Seven cohorts were evaluated using cross validation techniques, and 10 were studied in independent cohorts. Overall, 52.6% of patients were classified as high risk and 20.5% experienced disease recurrence. The false negative rate was > 20% in 8 studies (47%) and false positive rate was > 50% in 6 (35%). The number of genes in the assay correlated with assay sensitivity (r(sp)= 0.537; P = 0.032), the positive predictive value (r(sp) = 0.501; P = 0.048), and the diagnostic odds ratio (r(sp) = 0.532; P = 0.041). Conclusion: Gene expression profiles based on microarray analysis show early promise for predicting survival in patients with breast cancer. However, the use of these assays in therapeutic decision-making must consider the limitations of assay test performance and the specific patient population being evaluated.

L3 ANSWER 39 OF 47 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights

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ACCESSION NUMBER: 2006546626 EMBASE
TITLE: Genomics and proteomics of bone cancer.
AUTHOR: Marguiles A.G.; Klimberg V.S.; Bhattacharrya S.; Gaddy D.; Suva L.J.; Roodman; Berenson; Pearse; Vessella
CORPORATE SOURCE: L.J. Suva, Department of Physiology and Biophysics, University of Arkansas for Medical Sciences, Little Rock, AR 72205, United States. suvalarryj@uams.edu
SOURCE: Clinical Cancer Research, (15 Oct 2006) Vol. 12, No. 20 PART 2, pp. 6217s-6221s. .
Refs: 44
ISSN: 1078-0432 CODEN: CCREF4
COUNTRY: United States
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 016 Cancer
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 21 Nov 2006
Last Updated on STN: 21 Nov 2006

AB Although the control of bone metastasis has been the focus of intensive investigation, relatively little is known about the molecular mechanisms that regulate or predict the process, even though widespread skeletal dissemination is an important step in the progression of many tumors. As a result, understanding the complex interactions contributing to the metastatic behavior of tumor cells is essential for the development of effective therapies. Using a state-of-the-art combination of gene expression profiling and functional annotation of human tumor cells, and surface-enhanced laser desorption/ ionization time-of-flight mass spectrometry of patient serum, we have shown that changes in tumor biochemistry correlate with disease progression and help to define the aggressive tumor phenotype. Based on these approaches, it is apparent that the metastatic phenotype of tumor cells is extremely complex. The identification of the phenotype of tumor cells has benefited greatly from the application of gene expression profiling (microarray analysis). This technology has been used by many investigators to identify changes in gene expression and cytokine and growth factor elaboration (such as interleukin 8). The tumor phenotype(s) presumably also include changes in the cell surface carbohydrate profile (via altered glycosyltransferase expression) and heparan sulfate expression (via increased heparanase activity), to name but a few. These specific alterations in gene expression, identified by functional annotation of accumulated microarray data, have been validated using a variety of approaches. Collectively, the data described here suggest that each of these activities is associated with distinct aspects of the aggressive tumor cell phenotype. Collectively, the data suggest that multiple factors constitute the complex phenotype of metastatic tumor cells. In particular, the differences observed in gene expression profiles and serum protein biomarkers play a critical role in defining the mechanisms responsible for bone-specific colonization and growth of tumors in bone. Future studies will identify the mechanisms that participate in the formation of secondary tumor growths of cancers in bone. .COPYRGT. 2006 American Association for Cancer Research.

L3 ANSWER 40 OF 47 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 2006441023 EMBASE
TITLE: Gene expression profile of idiopathic thrombocytopenic purpura (ITP).
AUTHOR: Sood R.; Wong W.; Jeng M.; Zehnder J.L.
CORPORATE SOURCE: Dr. J.L. Zehnder, Department of Pathology, Stanford University School of Medicine, 300 Pasteur Drive, Stanford,

CA 94305-5324, United States. zehnder@stanford.edu
SOURCE: Pediatric Blood and Cancer, (15 Oct 2006) Vol. 47, No. 5 SUPPL., pp. 675-677. .
Refs: 14
ISSN: 1545-5009 E-ISSN: 1545-5017 CODEN: PBCEAQ
COUNTRY: United States
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 007 Pediatrics and Pediatric Surgery
025 Hematology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 5 Oct 2006
Last Updated on STN: 5 Oct 2006

AB To search for novel mechanisms that contribute to the pathophysiology of idiopathic thrombocytopenic purpura (ITP), we determined the whole blood gene expression profile in five ITP patients and five control samples. Using DNA microarrays that contained 24,473 unique putative genes, we found 176 cDNAs that were strongly correlated with ITP. These included a cluster of interferon-regulated genes and TLR7, as well many less-well characterized genes which are candidates for further study. We believe this approach is likely to yield new insights into our understanding of the molecular pathophysiology of ITP. .COPYRGT. 2006 Wiley-Liss, Inc.

L3 ANSWER 41 OF 47 EMBASE
ACCESSION NUMBER: 2006122027 EMBASE
TITLE: Identification and functional analysis of damage-induced neuronal endopeptidase (DINE), a nerve injury associated molecule.
AUTHOR: Kiryu-Seo S.
CORPORATE SOURCE: S. Kiryu-Seo, Department of Anatomy and Neurobiology, Osaka City University, Graduate School of Medicine, 1-4-3 Asahimachi, Abeno-ku, Osaka 545-8585, Japan. skiryu@med.osaka-cu.ac.jp
SOURCE: Anatomical Science International, (2006) Vol. 81, No. 1, pp. 1-6. .
Refs: 30
ISSN: 1447-6959 E-ISSN: 1447-073X CODEN: ASINC5
COUNTRY: Australia
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 005 General Pathology and Pathological Anatomy
008 Neurology and Neurosurgery
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 28 Mar 2006
Last Updated on STN: 28 Mar 2006

AB Nerve regeneration is a complex process associated with the expression of hundreds of genes. To elucidate the molecular mechanism responsible for nerve regeneration, hundreds of nerve regeneration-associated genes have been hunted using differential display polymerase chain reaction (DD-PCR), random cloning, microarray and proteomics. Damage-induced neuronal endopeptidase (DINE) is a newly identified nerve regeneration-related molecule derived from normal and axotomized hypoglosssal nuclei using DD-PCR. After full-length cloning, we have found that DINE is a neuron-specific membrane-bound metalloprotease. Damage-induced neuronal endopeptidase shares homology with neprilysin and endothelin-converting enzyme, which degrade or process neuropeptides. Although DINE has some neuroprotective effects, the physiological function of, as well as the substrate for, DINE remains obscure. The most intriguing property of DINE is its extreme transcriptional response against various types of nerve injuries,

including that of the peripheral and central nervous systems. Thus, a more detailed expression profile of DINE mRNA was investigated using the dorsal root ganglion (DRG) after sciatic nerve injury. In the DRG, DINE mRNA was observed in small-sized DRG neurons after axotomy. This expression profile was similar to that of the neuropeptide galanin. Both in vitro and in vivo studies revealed that leukemia inhibitory factor and nerve growth factor withdrawal additively enhanced the expression of DINE, as well as that of galanin. Damageinduced neuronal endopeptidase and galanin may use common transcriptional regulation machinery. Although functional correlation of these molecules remains unclear, their simultaneous induction may provide more successful protection for injured neurons.

L3 ANSWER 42 OF 47 EMBASE

ACCESSION NUMBER: 2005531984 EMBASE

TITLE: Genomic and gene expression signature of the pre-invasive testicular carcinoma in situ.

AUTHOR: Almstrup K.; Ottesen A.M.; Sonne S.B.; Hoei-Hansen C.E.; Leffers H.; Rajpert-De Meyts E.; Skakkebaek N.E.

CORPORATE SOURCE: K. Almstrup, University Department of Growth and Reproduction, Rigshospitalet, Blegdamsvej 9, 2100 Copenhagen, Denmark. kristian@almstrup.net

SOURCE: Cell and Tissue Research, (2005) Vol. 322, No. 1, pp. 159-165. .
Refs: 45
ISSN: 0302-766X CODEN: CTSRCS

COUNTRY: Germany
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 005 General Pathology and Pathological Anatomy
016 Cancer
022 Human Genetics
028 Urology and Nephrology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 22 Dec 2005
Last Updated on STN: 22 Dec 2005

AB Testicular cancer is the most common malignancy among men in the reproductive age and the incidence is increasing, probably caused by environmental factors. Most testicular cancers are testicular germ cell tumours and all originate from a carcinoma in situ (CIS) pattern. In this review, we focus on the pre-invasive CIS and its possible fetal origin by reviewing recent data originating from DNA microarrays and comparative genomic hybridisations. A comparison of gene expression and genomic aberrations reveal chromosomal "hot spots" with mutual clustering of gene expression and genomic amplification. Some of the genes found in the hot spots may be involved in creating the CIS phenotype. On the other hand, many genes that are highly expressed in CIS are not present in the hot-spot areas. The gene expression profile of CIS thus most likely reflects the combined result of genomic amplification and increased transcriptional activation and/or deficiency in the epigenetic silencing of specific loci. Amplification of chromosome 12p, appears to be a good genomic marker of the transition from the pre-malignant to malignant CIS cell; this is consistent with recent findings of propagation advantages in cultured undifferentiated embryonic stem cells after spontaneous amplification in similar regions. The gene expression profile of CIS cells has remarkable similarity to that of embryonic stem cells and supports our long-standing hypothesis of an early developmental origin of CIS and testicular germ cell cancer.

L3 ANSWER 43 OF 47 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 2005430831 EMBASE
TITLE: A gene expression fingerprint of C. elegans embryonic motor neurons.
AUTHOR: Fox R.M.; Von Stetina S.E.; Barlow S.J.; Shaffer C.; Olszewski K.L.; Moore J.H.; Dupuy D.; Vidal M.; Miller III D.M.
CORPORATE SOURCE: D.M. Miller III, Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN 37232-8240, United States. david.miller@vanderbilt.edu
SOURCE: BMC Genomics, (21 Mar 2005) Vol. 6, pp. 23p. .
Refs: 107
ISSN: 1471-2164 CODEN: BGMEET
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 008 Neurology and Neurosurgery
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 13 Oct 2005
Last Updated on STN: 13 Oct 2005

AB Background: Differential gene expression specifies the highly diverse cell types that constitute the nervous system. With its sequenced genome and simple, well-defined neuroanatomy, the nematode C. elegans is a useful model system in which to correlate gene expression with neuron identity. The UNC-4 transcription factor is expressed in thirteen embryonic motor neurons where it specifies axonal morphology and synaptic function. These cells can be marked with an unc-4::GFP reporter transgene. Here we describe a powerful strategy, Micro-Array Profiling of C. elegans cells (MAPCeL), and confirm that this approach provides a comprehensive gene expression profile of unc-4::GFP motor neurons in vivo. Results: Fluorescence Activated Cell Sorting (FACS) was used to isolate unc-4::GFP neurons from primary cultures of C. elegans embryonic cells. Microarray experiments detected 6,217 unique transcripts of which .apprx.1,000 are enriched in unc-4::GFP neurons relative to the average nematode embryonic cell. The reliability of these data was validated by the detection of known cell-specific transcripts and by expression in UNC-4 motor neurons of GFP reporters derived from the enriched data set. In addition to genes involved in neurotransmitter packaging and release, the microarray data include transcripts for receptors to a remarkably wide variety of signaling molecules. The added presence of a robust array of G-protein pathway components is indicative of complex and highly integrated mechanisms for modulating motor neuron activity. Over half of the enriched genes (537) have human homologs, a finding that could reflect substantial overlap with the gene expression repertoire of mammalian motor neurons. Conclusion: We have described a microarray-based method, MAPCeL, for profiling gene expression in specific C. elegans motor neurons and provide evidence that this approach can reveal candidate genes for key roles in the differentiation and function of these cells. These methods can now be applied to generate a gene expression map of the C. elegans nervous system. .COPYRGT. 2005 Fox et al; licensee BioMed Central Ltd.

L3 ANSWER 44 OF 47 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 2005182971 EMBASE
TITLE: Gene expression profiles in psoriasis: Analysis of impact of body site location and clinical severity.

AUTHOR: Quekenborn-Trinquet V.; Fogel P.; Aldana-Jammayrac O.; Ancian P.; Demarchez M.; Rossio P.; Richards H.L.; Kirby B.; Nguyen C.; Voegel J.J.; Griffiths C.E.M.

CORPORATE SOURCE: J.J. Voegel, Galderma R and D, 635 route des Lucioles, 06902 Sophia-Antipolis Cedex, France. johannes.voegel@galderma.com

SOURCE: British Journal of Dermatology, (2005) Vol. 152, No. 3, pp. 489-504. .
Refs: 80
ISSN: 0007-0963 CODEN: BJDEAZ

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; General Review

FILE SEGMENT: 013 Dermatology and Venereology
022 Human Genetics

LANGUAGE: English

SUMMARY LANGUAGE: English

ENTRY DATE: Entered STN: 19 May 2005
Last Updated on STN: 19 May 2005

AB Background: Psoriasis is characterized by symmetry of plaques and modulation of multiple genes within those plaques. Objectives: We compared gene expression profiles of plaques of psoriasis at different anatomical sites for both symmetrical and asymmetrical disease to ascertain whether the same genes were expressed. Methods: Gene expression profiles were analysed in biopsies from lesional and uninvolved skin from two groups of patients with either predominantly symmetrical or truncal plaques of psoriasis vulgaris, and from normal skin of healthy volunteers. Genomic analyses were performed using cDNA array and kinetically monitored reverse transcriptase-initiated polymerase chain reaction (kRT-PCR) approaches. A cluster of genes upregulated in involved psoriasis skin as compared with normal skin was identified using each of these two technologies. Results: Clustering of patients based on their gene expression profile did not reveal any correlation with family history of psoriasis, age at onset or association of psoriasis with arthritis. There was no difference in gene expression profile between the type (symmetrical vs. truncal) or location (left vs. right side of body) of psoriatic plaques. Gene expression profiles of involved psoriatic skin analysed by kRT-PCR analysis did correlate with both global (Psoriasis Area and Severity Index) and local (erythema, desquamation and plaque elevation) clinical severity. Conclusions: These results indicate that it may be feasible to analyse the molecular effects of pharmacological agents on psoriatic skin in 'minizone' protocols, that the obtained data can be correlated with clinical severity and that plaques of psoriasis in the same individual express the same genes. .COPYRGT. 2005 British Association of Dermatologists.

L3 ANSWER 45 OF 47 EMBASE

ACCESSION NUMBER: 2004497219 EMBASE

TITLE: Asiaticoside induction for cell-cycle progression, proliferation and collagen synthesis in human dermal fibroblasts.

AUTHOR: Lu L.; Ying K.; Wei S.; Fang Y.; Liu Y.; Lin H.; Ma L.; Mao Y.

CORPORATE SOURCE: Dr. L. Lu, State Key Lab. of Genet. Engineering, Institute of Genetics, Fudan University, Shanghai 200433, China. luluo@vip.163.com

SOURCE: International Journal of Dermatology, (2004) Vol. 43, No. 11, pp. 801-807. .
Refs: 23
ISSN: 0011-9059 CODEN: IJDEBB

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 013 Dermatology and Venereology
022 Human Genetics
030 Pharmacology
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 9 Dec 2004
Last Updated on STN: 9 Dec 2004

AB Asiaticoside, isolated from Centella asiatica, promotes fibroblast proliferation and extracullar matrix synthesis in wound healing. The precise mechanism, however, in molecular and gene expression levels still remains partially understood. Using cDNA microarray technology, the alternation of genes expression profiles was determined in a human dermal fibroblast in vitro in the presence of asiaticoside (30 μg/ml). Fifty-four genes, with known functions for cell proliferation, cell-cycle progression and synthesis of the extracellular matrix, were significantly up-regulated in our "whole-genes nest" expression profile at various timepoints. Furthermore, mRNA levels and protein productions of certain genes responsible for extracellular matrix (ECM) synthesis (e.g. encoding type I and type III collagen proteins) were evaluated by Northern blot and radioimmunoassay, respectively. As a result, there is a close correlation among the gene profile, mRNA and protein production in the cells response to asiaticoside stimulation. This information could be used for exploring the target genes in response to asiaticoside in fibroblasts. .COPYRGT. 2004 The International Society of Dermatology.

L3 ANSWER 46 OF 47 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 2004354181 EMBASE
TITLE: How much expression divergence after yeast gene duplication could be explained by regulatory motif evolution?.
AUTHOR: Zhang Z.; Gu J.; Gu X.
SOURCE: Trends in Genetics, (2004) Vol. 20, No. 9, pp. 403-407. .
Refs: 36
ISSN: 0168-9525 CODEN: TRGEE2
PUBLISHER IDENT.: S 0168-9525(04)00186-6
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 2 Sep 2004
Last Updated on STN: 2 Sep 2004

AB We used the yeast genome sequences of gene families, microarray profiles and regulatory motif data to test the current wisdom that there is a strong correlation between regulatory motif structure and gene expression profile. Our results suggest that duplicate genes tend to be co-expressed but the correlation between motif content and expression similarity is generally poor, only .apprx.2-3% of expression variation can be explained by the motif divergence. Our observations suggest that, in addition to the cis-regulatory motif structure in the upstream region of the gene, multiple trans-acting factors in the gene network can influence the pattern of gene expression significantly. .COPYRGT. 2004 Elsevier Ltd.

L3 ANSWER 47 OF 47 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 2004293117 EMBASE

TITLE: Customized antigens for desensitizing allergic patients.
AUTHOR: Ferreira F.; Wallner M.; Thalhamer J.
CORPORATE SOURCE: F. Ferreira, University of Salzburg, Department of Molecular Biology, Salzburg, Austria
SOURCE: Advances in Immunology, (2004) Vol. 84, pp. 79-129. .
Refs: 215
ISSN: 0065-2776 CODEN: ADIMAV
PUBLISHER IDENT.: S 0065-2776(04)84003-3
COUNTRY: United States
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 026 Immunology, Serology and Transplantation
037 Drug Literature Index
038 Adverse Reactions Titles
039 Pharmacy
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 5 Aug 2004
Last Updated on STN: 5 Aug 2004

AB Molecular cloning and recombinant production of allergens opened new possibilities for the increasing problem of allergies. The concept of molecule-based instead of allergen extract-based diagnosis was developed and is already being implemented in the field. Molecule-based diagnosis allows not only the precise identification of allergen recognition patterns of individual patients and the quantification of IgE levels to each allergen, but it might also help to predict potential sensitization to multiple allergenic sources resulting from the cross-reactivity phenomenon. Information about the sensitization profile of individual patients forms the basis for the development of customized forms of immunotherapy based on the use of recombinant and synthetic protein antigens. For this purpose, a variety of preparations are being developed for different allergies. Major goals are to increase safety by minimizing the risk of IgE-mediated side effects and to improve efficacy of specific immunotherapy by counterbalancing the ongoing Th2-biased allergic response. Synthetic peptides in question are mimotopes, such as artificial peptide structures mimicking IgE binding epitopes, B-cell epitope-derived peptides, and T-cell epitope-containing peptides. Recombinant-based approaches are mostly focused on genetic engineering of allergens to produce molecules with reduced allergenic activity and conserved antigenicity, such as hypoallergens. An alternative to genetic engineering is the chemical modification of pure allergens with immunostimulatory DNA sequences (allergen-ISS conjugates), which mask IgE epitopes and add a desirable Th1-inducing character to the allergen molecule. Several of these customized allergen preparations have been already evaluated for their safety in clinical provocation studies. So far, clinical trials showed the efficacy and safety of immunotherapy with T-cell epitope-containing peptides and with allergen-ISS conjugates for cat-allergic and ragweed pollen-allergic patients, respectively. In addition, two preparations consisting of hypoallergenic derivatives are being evaluated for immunotherapy of birch pollen-allergic patients. In parallel, several animal studies have now demonstrated the potential of genetic immunization for allergy treatment in the future. The antiallergic effect of DNA vaccines translating wild-type allergen genes or hypoallergenic derivatives is attributed to the recruitment of Th1 cells and the establishment of a balancing Th1-biased cytokine environment.

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(FILE 'HOME' ENTERED AT 14:06:06 ON 12 APR 2007)

FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE' ENTERED AT 14:08:17 ON 12 APR 2007

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L1          193 GENE AND PROFILE AND EXPRES? AND CORREL? AND REVIEW
L2          133 DUP REM L1 (60 DUPLICATES REMOVED)
L3           47 (ARRAY OR ?ARRAY) AND L2

=> logoff hold
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                      ENTRY     SESSION
FULL ESTIMATED COST                                   160.34      161.18

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                      ENTRY     SESSION
CA SUBSCRIBER PRICE                                   -19.50      -19.50

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STN INTERNATIONAL SESSION SUSPENDED AT 14:11:50 ON 12 APR 2007
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